

# and proceedings to the control SEQUENCE LISTING

<110>	Rouquier, Sylvie	
	Giorgi, Dominique	

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Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser 170 165

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Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His

Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val 75

Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys 105

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 120

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu 130

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys

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Val Met Tyr Thr Val Val Thr Pro

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180 185 190

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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Ser Leu His 50 55 60

Tyr Thr Val Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Leu Gly 65 70 75 80

Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val 85 90 95

Leu Arg Leu Ser Phe Cys Ile Lys Met Glu Ile Pro His Phe Phe Cys 100 105 110

Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn 115 120 125

Asn Val Val Ile Tyr Phe Ala Thr Gly Ile Leu Ala Val Ile Pro Phe 130 135 140

Thr Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Phe Ser Val Leu Arg 145 150 155 160

Ile Ser Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175 His Leu Ser Met Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 190

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Ser Leu Gln Thr Arg Ser Lys Ala Ile Ser Tyr Pro Cys Cys Leu Thr
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Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Ile Ile Ile
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Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Val
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Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His Tyr Phe Cys
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gtc ccc tc Val Pro Se	gca ggc Ala Gly 165	ggc agg Gly Arg	aag aaa Lys Lys	gcc ttc Ala Phe 170	tcc acc Ser Thr	tgc ag Cys Se 17	r Ser	529
cac ctg to His Leu Se	gtg gtt Val Val 180	gct.ctc Ala Leu	ttc tat Phe Tyr 185	ggg acc Gly Thr	acc att Thr Ile	ggt gt Gly Va 190	c tat 1 Tyr	577
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Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val

Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys 100

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn 120

Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Gly Gly Ala Leu 135

Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Gly 155

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acc g Thr V 5	tg al 1	atg Met	gcc Ala	ttt Phe	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His		193
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acc t Thr S	cg Ser	tca Ser	gct Ala	cag Gln 165	Gly	aag Lys	tac Tyr	aag Lys	gca Ala 170	Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	Ser		529
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Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
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Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
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170

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481

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Glu	Va]		: Ile	e Met	. Val	l Ser		: Ile	e Val	l Leu	Let 140	ı Met	Th	r Pro	o Leu		

Cys Leu Val 145	Leu Leu	Ser T	yr Il	e Arg		le S 155	er T	hr I	le I	Leu	Lys 160	
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Ile His Pro 195	His Ser	Ser I	Pro Se 20	r Val 0	Leu (	Gln G	Slu I 2	ys 1 205	Leu	Ile	Ser	
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115 120 125	
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Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ile Leu Lys 155

Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe Ser Thr Arg Ser Ser

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Gln V		Tyr 35	Phe	Ser	Met	Leu	Phe 40	Pro	lle	Leu	Asp	Thr 45	Leu	Leu	Leu	
Thr '	Val 1 50	Met	Ala	Tyr	Asp	Arg 55	Phe	· Val	Ala	Ile	Cys 60	Leu	Pro	Leu	His	
Tyr l					_	_	•			<b>01.</b>			т16	Dho	เบาไ	

Ile Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met 85 90 95

Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val Phe Pro Leu 130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys 145 150 155 160

Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His 180  $\,$  185  $\,$  190  $\,$ 

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Val Met Tyr Thr Val Val Thr Pro 210 215

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  Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
 aac ttg gtt gtg gaa tat aga act att tcc ttc aca gga tgc atc atg
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 Asn Leu Val Val Glu Tyr Arg Thr Ile Ser Phe Thr Gly Cys Ile Met
                                                     3.0
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tac Tyr 65	aca Thr	gtt Val	gca Ala	atg Met	tcc Ser 70	cag Gln	agg Arg	ctt Leu	tgc Cys	tcc Ser 75	ttg Leu	ttg Leu	gtg Val	gct Ala	aca Thr 80	241
tca Ser	.tac Tyr	tct Ser	tgg Trp	85 85	ata Ile	gtc Val	tgt Cys	ttc Phe	ctg Leu 90	aca Thr	ctt Leu	acc Thr	tac Tyr	ttt Phe 95	cta Leu	289
ctg Leu	gaa Glu	tta Leu	tcc Ser 100	ttc Phe	aga Arg	gga Gly	aat Asn	aat Asn 105	atc Ile	att Ile	aat Asn	aac Asn	ttt Phe 110	gtc Val	tgt Cys	337
gag Glu	cat His	gct Ala 115	gcc Ala	att Ile	gtt Val	gct Ala	gtg Val 120	tct Ser	tgc Cys	tct Ser	gac Asp	ccc Pro 125	tat Tyr	gtg Val	agc Ser	385
cag Gln	gag Glu 130	atc Ile	act Thr	tta Leu	gtt Val	tct Ser 135	gcc Ala	aca Thr	ttc Phe	aat Asn	gaa Glu 140	ata Ile	agc Ser	agt Ser	ctg Leu	433
atg Met 145	atg Met	att Ile	ttc Phe	act Thr	tcc Ser 150	tat Tyr	gct Ala	ttc Phe	att Ile	ttt Phe 155	atc Ile	act Thr	gtc Val	atg Met	aag Lys 160	481
atg Met	cct Pro	tcc Ser	act Thr	999 Gly 165	999 999	cgc Arg	aag Lys	aaa Lys	gcg Ala 170	ttc Phe	tcc Ser	acg Thr	tgt Cys	gcc Ala 175	tcc Ser	529
cac His	ctg Leu	acc Thr	gcc Ala 180	att Ile	acc Thr	att Ile	ttc Phe	cat His 185	Gly aaa	act Thr	atc Ile	ctt Leu	ttc Phe 190	ctc Leu	tac Tyr	577
tgt Cys	gtt Val	cct Pro 195	Asn	tcc Ser	aaa Lys	agt Ser	tca Ser 200	tgg Trp	ctc Leu	atg Met	gtc Val	aag Lys 205	gtg Val	acc Thr	tct Ser	625
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Gln Phe Phe Leu Val Cys Ile Phe Val Gly Thr Glu Thr Phe Met Leu

Ala Val Met Ala Tyr Asp Arg Cys Val Ala Val Cys Asn Pro Leu Leu 60 50 55

Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Thr

Ser Tyr Ser Trp Gly Ile Val Cys Phe Leu Thr Leu Thr Tyr Phe Leu

Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys

Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Val Ser

Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu 130

Met Met Ile Phe Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys 150 145

Met Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser 170 165

His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr 185

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tcccccatct tgcatgttgt gacagcatca ccaataacgt catcatgtat ttccctgctg
                                                                     420
ccgtatttgg tttccttccc atctcgggga cccttttctc ttgctataaa atcgtttcct
                                                                     480
ccattctgag ggtttcatca tcaggtggga ggtataaagc cttctccacc tgtgggtctc
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acctgtcagt tgtttgctga gtttatggaa gaggtgttgg agggtacctc agttcaggtg
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                                                                      180
tetgtcacce tetatategt teagecatea tgaateegtg tttetgtgge tacetagttt
                                                                      240
tgttgtcttt ttttttttc ttcgcagtcg tttagactcc cagctgcaca acttgattgc
                                                                      300
                                                                      360
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                                                                      420
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                                                                     300
                                                                     360
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teteaactee eccatettge atgttgtgae acetteacea ggaacateaa eetgtattte
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<sup>&</sup>lt;211> 649

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acc Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgʻt Cys 60	cac His	cct Pro	ctg Leu	cac His	193
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atc Ile	tca Ser	tca Ser	gct Ala	cag Gln 165	Gly aaa	aag Lys	tat Tyr	aag Lys	gca Ala 170	Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser	529
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Gln Met Cys Phe Phe Leu Leu Phe Val Gly Leu Asp Asn Phe Leu Leu

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 55

Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Ile Val Gly Val Leu Asn Ser Met Leu Gln Ser Leu Met Val

Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His Phe Phe Cys

Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn 120 115

Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly Pro Leu 135 130

Asn Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 155

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170

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Val Met Tyr Thr Val Val Thr Pro

215

ctg agt tot gct gtg acc cat tot too cag agc agc too atg gcc toa Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser 200

gtg atg tac gcc atg gtc acc ccc Val Met Tyr Ala Met Val Thr Pro

649

625

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Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Val Leu Leu Met 90

Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys 100

Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn

Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val

Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg

Thr Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 170 165

His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr \$180\$ \$185\$ \$190

Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser 195 200 205

Val Met Tyr Ala Met Val Thr Pro 210 215

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Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Leu Cys Cys Ile Cys Ser

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135

130

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His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Val Gly Val Tyr
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cag gtg tat ttt tta atg atg ttt gct gga atg gat act ttc cta ctg
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Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
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                                                                            193
 gee gtg atg gee tat gae egg ttt gtg gee ate tge eac eec etg eac
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
tac acg gtc atc atg aac ccc tgc ctc tgt ggc ctc ctg gtt ctg gca
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 Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala
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 Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile Leu Leu Met
 aag aag ttg acc ttc tcc aca ggc act gag att ccg cat ttc ttc tgt
                                                                            337
 Lys Lys Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
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 gaa ccg gct cag gtc ctc aag gtg gcc tgc tct aac acc ctc ctc aat
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115 120 125

115 120 125	
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acg tcc tcc acc gag ggc aag tac aaa gcc ttt tcc acg ctg tgg atc 529 Thr Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Leu Trp Ile 165 170 175	
tcc ctc tgt gtg gtc tcc ttg ttc tat gga aca gga ctt ggg gtc tat 577 Ser Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 190	
ctg agt tct gct gtg acc cac tct tcc cag agc agc tcc atg gcc tca 625 Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser 195 200 205	
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Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His	
50 55 60	
Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala	

Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn 115  Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val 135  Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg 150	
Thr Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Leu Trp Ile 175 170 165  Ser Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 185	
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aat ata ctg aca cag aac aaa ttc ata aca tat gca ggc tgt ctc ggt
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Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr Ala Gly Cys Leu Gly
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cag att ttt ttt ttc act tca ttt gga tgc ctg gac aat tta ctc ttg
Gln Ile Phe Phe Phe Thr Ser Phe Gly Cys Leu Asp Asn Leu Leu Leu
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act gtg atg gcc tat gac cgc ttc gtg gcc atc tgt cac ccc ctg cac
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
                                             60
 tat acg gtc atc atg aac ccc cgg ctc tgt gga ctg ctg gtt ctg ggg
                                                                       241
 Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Gly
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Ile	Ser	Ser	Ala	Gly 165	Arg	Lys	His	Lys	Ala 170	Phe	Ser	Thr	Cys	Gly 175	Ser		
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Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg

Tyr Ala Val Ile Met Asn Leu Arg Leu Cys Gly Phe Leu Ile Leu Leu 70

Ser Leu Ser Ile Ser Ile Met Asp Thr Leu Leu His Asp Leu Met Val

Leu Arg Leu Ser Phe Cys Thr His Leu Glu Ile Pro Leu Phe Phe Cys

Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr Leu Ile Asn 120

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Ser Gly Ile Ile Phe Ser Tyr Thr Gln Ile Ala Ser Ser Val Leu Arg 145

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gtcgtctcct tattttattg tacatgccta ggggtgtacc tcagttctgc tacacacaac
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cag Gln	gtg Val	tat Tyr 35	ttt Phe	ttt Phe	atg Met	att Ile	ttt Phe 40	gct Ala	gga Gly	ctg Leu	gat Asp	aat Asn 45	ttc Phe	ctc Leu	ctg Leu	,	145
acc Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgc Cys 60	cac His	ccc Pro	ctg Leu	cac His		193
tac Tyr 65	atg Met	gtc Val	atc Ile	atg Met	aat Asn 70	ccc Pro	cgc Arg	ttc Phe	tgt Cys	gcc Ala 75	ctc Leu	ctg Leu	gtt Val	ctc Leu	atg Met 80	;	241
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atg Met	tcc Ser	tcc Ser	act Thr	tca Ser 165	gca Ala	aag Lys	aat Asn	aaa Lys	gca Ala 170	Phe	tcc Ser	acc Thr	tgt Cys	999 Gly 175	Ser		529
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ctc Leu	agc Ser	tct Ser 195	Ala	gtg Val	acc Thr	cct Pro	tct Ser 200	Ser	cag Gln	agc Ser	agc Ser	gcc Ala 205	Ile	gcc Ala	tca Ser		625
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Met Val Ile Met Asn Pro Arg Phe Cys Ala Leu Leu Val Leu Met 65 70 75 80

Ser Trp Phe Ile Met Ser Leu Val Ala Leu Val His Val Leu Leu Ile 85 90 95

Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Ser Cys 100 105 110

Glu Val Ala Gln Ile Leu Lys Val Ala Arg Ser Asp Thr Phe Phe Asn 115 120 125

Asn Ile Cys Leu Tyr Leu Ser Ala Val Leu Leu Gly Val Phe Pro Val 130 135 140

Met Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg 145 150 155 160

Met Ser Ser Thr Ser Ala Lys Asn Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

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Val Gln Thr Trp Ser Lys Val Ile Ser Tyr Thr Gly Cys Ile Thr Gln
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Met Asp Phe Phe Leu Leu Phe Val Gly Leu Asp Asn Phe Leu Leu Thr
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Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr
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cgg Arg	cta Leu	acc Thr	ttc Phe 100	tgt Cys	aca Thr	gac Asp	ttg Leu	gaa Glu 105	atc Ile	ccc Pro	cac His	ttt Phe	ttc Phe 110	tgt Cys	gaa Glu	337
ctt Leu	aat Asn	cag Gln 115	ata Ile	atc Ile	cac His	ctt Leu	gcc Ala 120	tgt Cys	tcg Ser	gac Asp	acc Thr	ttt Phe 125	ctt Leu	aat Asn	gac Asp	385
gtg Val	gtg Val 130	atg Met	tat Tyr	ttg Leu	gca Ala	gtg Val 135	atg Met	ctg Leu	ctg Leu	ggt Gly	999 Gly 140	gga Gly	tgc Cys	ctt Leu	act Thr	433
999 Gly 145	atc Ile	ctt Leu	tac Tyr	tct Ser	tac Tyr 150	tct Ser	aag Lys	ata Ile	gtt Val	tcc Ser 155	tcc Ser	gta Val	cgt Arg	gca Ala	atc Ile 160	481
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agt Ser	tct Ser	gct Ala 195	aca Thr	cac His	aac Asn	tca Ser	cac His 200	tcc Ser	agc Ser	gca Ala	aca Thr	gcc Ala 205	tcg Ser	gtg Val	atg Met	625
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Met	Asp	Phe 35	Phe	e Leu	Leu	Phe	Val	Gly	Leu	Asp	Asn	Phe 45	. Leu	Leu	Thr	
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Trp Ile Leu Ser Val Leu Asn Ser Leu Ser Gln Ser Leu Met Val Leu
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Arg Leu Thr Phe Cys Thr Asp Leu Glu Ile Pro His Phe Cys Glu
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                                105
Leu Asn Gln Ile Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn Asp
                            120
Val Val Met Tyr Leu Ala Val Met Leu Leu Gly Gly Cys Leu Thr
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Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala Ile
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                    150
Ser Ser Ala Gln Gly Lys Cys Lys Ala Phe Ser Thr Cys Ala Ser His
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Leu Leu Val Val Ser Leu Phe Tyr Cys Thr Cys Leu Gly Val Tyr Leu
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gcc Ala	tcc Ser 50	atg Met	gct Ala	att Ile	gac Asp	cgg Arg 55	ctg Leu	gtg Val	gcc Ala	atc Ile	tgc Cys 60	aaa Lys	ccc Pro	ttc Phe	cac His	193
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ctg Leu	tgc Cys	atc Ile	atc Ile	ttc Phe	tcc Ser	Tyr	ctg Leu	aga Arg	atc Ile	atc Ile 155	atc Ile	act Thr	gtg Val	ctc Leu	gca Ala 160	481

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Tyr Asp Val Val Met Ser Pro Arg Arg Cys Leu Leu Met Leu Leu Gly 65 70 75 80	
Ser Cys Thr Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met 85 90 95	
Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys His Phe Phe Cys 100 105 110	,
Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser 115 120 125	
Gln Ile Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe 130 135 140	
Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Ala	

160

49

Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser 170

155

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acc gtg atg gcc tat gac cgg ttt gtg gtc atc tgc cac cca ctg cac 193 Thr Val Met Ala Tyr Asp Arg Phe Val Val Ile Cys His Pro Leu His

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Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala 155

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165

His Leu Ala Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr 185 180

Leu Ser Ser Ala Ala Thr His Asn Ser His Ser Ser Ala Thr Ala Ser 200

Val Met Tyr Thr Val Val Thr Pro

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<211> 642

<212> DNA

<213> Eulemur rubriventer

<220>

misc\_feature <221>

(1)..(642) <222>

<223> Taxon = 34829; gene = EFU84; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127863

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<sup>73</sup> <210>

<sup>&</sup>lt;211> 652

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Eulemur fulvus

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= AF127864
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                                                                      120
tgcagggttg gatatcttta tgctgatcat gatggcctat gaccggtttg gggccatctg
                                                                      180
tcacccactg cagtacacgg tcatcatgaa ccccaggete tgtgggetge tggttgtggt
                                                                      240
gccctggatc ttgagtgacc tgaattcctt gttacaaagc ttaatggtgt tgtcactgtc
                                                                      300
cttttgtaga cacttggaaa tcctcacttt ttctgtgaac ttaatcaggt tgtccacctt
                                                                      360
gcctgttctg aaaccttctt taatgacatg gtgatgtatc tgatatctgt ggtgctgggt
                                                                      420
ggtggttccc tggctgggac tctttattct ttcttactgc agaatagttt gctccatacg
                                                                      480
tgcaacgtcc tcagctcagg ggaagtataa agcatttccc acctgtgcat ctcacctctc
                                                                      540
agttgtctcc ttatcttcct gcacaatcct aggggtgtac ctcagctctg ctgctaccca
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                                                                      652
gaattcgtgc tccagtgcag tagccttggt ggtgtacacg gtggtcactc cc
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       74
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       649
<212>
       DNA
       Eulemur fulvus
<213>
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       misc feature
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  Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val
                                                                        97
aac att gaa aca cac agc aaa gac atc tcc tac atg gga tgc ctc act
Asn Ile Glu Thr His Ser Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
                                                                       145
cag atg tat ttt ttc atg att ttt gct gga ctg gat aat ttc ctc ctg
Gln Met Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu
                             40
                                                                       193
 act gtg atg gcc tat gac cgg ttt gtg gcc atc tgc cac ccc tta cac
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
                                             60
                                                                       241
 tac acg gtc atc atg agt ccc cgc ttc tgt gcc ctc ctg gtt ctc ata
Tyr Thr Val Ile Met Ser Pro Arg Phe Cys Ala Leu Leu Val Leu Ile
                                                              80
                                         75
                     70
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tct tgg ttc a Ser Trp Phe I	itc atg lle Met 85	acc ctg Thr Leu	gtt go Val Al	cc ctg la Leu 90	gtt Val	cat His	gta Val	cta Leu	ctg Leu 95	ata Ile	289
ttg agg ctg a Leu Arg Leu T	acc ttc Thr Phe	tct tta Ser Leu	gaa ac Glu Th	ır Glu	atc Ile	cca Pro	cat His	ttc Phe 110	ttc Phe	tgt Cys	337
gac ctg gct c Asp Leu Ala G 115	ag att In Ile	ctc gag Leu Glu	gtg go Val Al 120	cc cac la His	tct Ser	Asp	acc Thr 125	ctc Leu	atc Ile	aat Asn	385
aac atc tgc a Asn Ile Cys M 130	atg tac Met Tyr	ttg tcg Leu Ser 135	act gt Thr Va	tg ttg al Leu	Leu	ggc Gly 140	gtg Val	ttt Phe	cct Pro	gtc Val	433
acg ggg atc o Thr Gly Ile I 145	ctc ttc Leu Phe	tcc tac Ser Tyr 150	tct as	aa att ys Ile	gtc Val 155	tcc Ser	tcc Ser	tta Leu	atg Met	agg Arg 160	481
atg tcc tcc a Met Ser Ser 1	act gca Thr Ala 165	ggc aag Gly Lys	aag aa Lys Ly	aa gca ys Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	ggg Gly 175	tct Ser	529
cac ctc tct o	gtg gtc Val Val 180	tgc ttg Cys Leu	Phe C	gc gga ys Gly 85	aca Thr	gga Gly	gtt Val	999 Gly 190	gtc Val	tat Tyr	577
ctc agt tct o Leu Ser Ser i 195	gct gtg Ala Val	acc cct Thr Pro	tct to Ser So 200	cc cag er Gln	agc Ser	agc Ser	agc Ser 205	att Ile	gcc Ala	tca Ser	625
gtg atg ttc a Val Met Phe '	acg gtg Thr Val	gtc acc Val Thr 215	ccc Pro								649
<210> 75 <211> 216 <212> PRT <213> Eulem	ur fulvı	ıs									
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Asn Ile Glu	Thr His 20	Ser Lys		le Ser 25	Tyr	Met	Gly	Cys	Leu	Thr	
Gln Met Tyr 35	Phe Phe	Met Ile	Phe A	Ala Gly	Leu	Asp	Asn 45	Phe	e Lev	. Leu	
Thr Val Met 50	Ala Tyr	Asp Arg	g Phe V	/al Ala	lle	Cys 60	His	Pro	Leu	ı His	

Tyr Thr Val Ile Met Ser Pro Arg Phe Cys Ala Leu Leu Val Leu Ile

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65 7	70	75	80
Ser Trp Phe Ile Met T	Thr Leu Val Ala Leu '	Val His Val Leu Leu	Ile
85	90	95	
Leu Arg Leu Thr Phe S	Ser Leu Glu Thr Glu 105	Ile Pro His Phe Phe 110	Cys
Asp Leu Ala Gln Ile L	Leu Glu Val Ala His	Ser Asp Thr Leu Ile	Asn
115	120	125	
Asn Ile Cys Met Tyr L	Leu Ser Thr Val Leu	Leu Gly Val Phe Pro	Val
130	135	140	
Thr Gly Ile Leu Phe S	Ser Tyr Ser Lys Ile	Val Ser Ser Leu Met	Arg
145	150	155	160
Met Ser Ser Thr Ala G	Gly Lys Lys Lys Ala	Phe Ser Thr Cys Gly	Ser
165	170	175	
His Leu Ser Val Val (	Cys Leu Phe Cys Gly	Thr Gly Val Gly Val	Tyr .
180	185	190	
Leu Ser Ser Ala Val 1	Thr Pro Ser Ser Gln	Ser Ser Ser Ile Ala	Ser
195	200	205	
Val Met Phe Thr Val V 210	Val Thr Pro 215		
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tgctggaatg gatactttcc	tactggccat	gatggcctat	gaccggtttg	tggccatctg	180
ccacccctg cactacacgg	tcatcatgaa	cccctgcctc	tgtggcctcc	tggttctggc	240
atcttgattc atcattttat	gggtctccct	agttcatatt	ctactgatga	agagtttgat	300
ctccataggc actgagattc	cgcatttctt	ctgtgaactg	gctcaggtcc	tcaaggtggc	360
ccgctctgat actctcctcg	ttaacattgt	cttgtatgtg	gccacagcac	tgctgggtgt	420
gcttcctgta gctgggatcc	tcttctccta	ctctcagatc	gtctcctcct	taatgaggat	480

gree	tcca	.cc g	Jaggg	caag	ji gi	aaay	Judet		Cacc	Lyc	9990	ctca		ctgt	90990	310
ctcc	ttgt	tc t	atgg	aaca	ıg ga	cttg	gggt	cta	tata	agt	tctg	ctgt	ga c	ccat	tcttc	600
ccag	agca	.gc t	ccat	ggcc	t ca	ıgtga	tgta	cac	catg	gtc	accc	CC				646
<210> 77 <211> 649 <212> DNA <213> Macaca sylvanus																
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<220> <221> CDS <222> (2)(649) <223> Product = olfactory receptor																
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aac Asn	atc Ile	cag Gln	aca Thr 20	cag Gln	aac Asn	aaa Lys	gtc Val	atc Ile 25	acc Thr	tat Tyr	gca Ala	ggc Gly	tgc Cys 30	atc Ile	agc Ser	97
cag Gln	atg Met	tgc Cys 35	ttt Phe	ttc Phe	ata Ile	ttc Phe	ttt Phe 40	gca Ala	gga Gly	ttg Leu	gac Asp	atc Ile 45	ttt Phe	atg Met	ctg Leu	145
acc Thr	gtg Val 50	atg Met	gcc Ala	tac Tyr	gac Asp	agg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
tac Tyr 65	acg Thr	gtc Val	acc Thr	atg Met	aac Asn 70	ccc Pro	agg Arg	ctc Leu	tgt Cys	gga Gly 75	ctg Leu	ctg Leu	gtt Val	ctg Leu	gcg Ala 80	241
tcc Ser	tgg Trp	atc Ile	atg Met	agt Ser 85	gcc Ala	ctg Leu	aat Asn	tct Ser	tca Ser 90	ttg Leu	caa Gln	agc Ser	tta Leu	atg Met 95	gta Val	289
ttg Leu	cac His	ctt Leu	tcc Ser 100	ttc Phe	tgt Cys	gca Ala	gac Asp	ttg Leu 105	gaa Glu	att Ile	ccc Pro	cac His	ttt Phe 110	ttc Phe	tgt Cys	337
gaa Glu	ctt Leu	aat Asn 115	cag Gln	gtc Val	atc Ile	cac His	ctt Leu 120	acc Thr	tgt Cys	tct Ser	gac Asp	act Thr 125	ttt Phe	ctt Leu	aat Asn	385
gac Asp	atg Met 130	gtg Val	atg Met	tat Tyr	ttg Leu	tca Ser 135	gct Ala	gtg Val	ctg Leu	ctg Leu	ggt Gly 140	Gly ggg	gga Gly	tgt Cys	ctc Leu	433
att Ile 145	GJA aaa	atc Ile	ctt Leu	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	atc Ile	gtc Val 155	tcc Ser	tct Ser	ata Ile	cat His	gca Ala 160	481
atc	tca	tca	gtt	cag	ggg	aag	tac	aag	gca Ala	ttt	tcc Ser	acc Thr	tgt Cvs	gca Ala	tct Ser	529

165 170 175

cac ctc tcg gtt gtc tcc tta ttt tat tgt aca atc cta ggt gtg tac

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ile Leu Gly Val Tyr

180

185

190

625

ctt agt tct gct gca acc cac agc tca cac gca agt gct gca gtc tcg
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195 200 205

gtg atg tac act gtg gtt acc ccc

Val Met Tyr Thr Val Val Thr Pro
210
215

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<213> Macaca sylvanus

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Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val 85 90 95

Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Cys 100 105 110

Glu Leu Asn Gln Val Ile His Leu Thr Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asp Met Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Cys Leu 130 135 140

Ile Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile His Ala 145 150 155 160

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Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser Val 180 Val Ser Leu Phe Tyr 185 Cys Thr Ile Leu Gly Val Tyr 180 Ser Ser Ala Ala Thr His Ser Ser His Ala Ser Ala Ala Val Ser
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Val Met Tyr Thr Val Val Thr Pro 210 215

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<210> 79
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<223> Taxon = 9546; gene = MSY16; Accession DDBJ/EMBL/GenBank = AF127868
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<222> (2)..(649)
<223> Product = olfactory receptor
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                                       10
                                                                       97
aac atc cag gcg cag agc aat gcc atc agc tat gca ggc tgc atc tcc
Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser
            20
cag atg tat ttt ttc atg gtt ttt gga ggc ata gac aca ttt ctc ctc
                                                                       145
Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu
acc gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg tac
                                                                       193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
                        55
tac cct gtc att atg aac ccc cgc ctc tgt ggc ctg ctg gtt ctt gtg
                                                                       241
Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
 tee tgg tte etc age ttg tea tae tee etg ate eag agt etg ttg atg
                                                                       289
 Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
                                     90
                 85
 ctg cag ttg tcc ttt tgc acc agt tgg gtc att cag cac ttt tac tgc
                                                                       337
Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
             100
                                                                       385
 gag ctt gct cag gcc ctc acg ctt gcc tgc tca gac aca cac atc aat
 Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn
                             120
                                                                       433
 tac atc ctg ctc tac gtg gtg acc ggc ctt ctg ggt ttt gtg ccc ttc
 Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe
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130 135 140

		135					140					
tca gga atc Ser Gly Ile 145	ctt ttc Leu Phe	tcc tac Ser Tyr 150	acc Thr	caa Gln	Ile V	gtc   Val   155	tcc Ser	tcc Ser	atc Ile	ctg Leu	aga Arg 160	481
atc tca tcc Ile Ser Ser	aca gat Thr Asp 165	ggg aaa Gly Lys	cac His	Lys .	gcc ( Ala 1 170	ttt Phe	tct Ser	aac Asn	tgc Cys	gga Gly 175	tct Ser	529
cat ctg tct His Leu Ser	gtg gtt Val Val 180	ttt tta Phe Leu	ttc Phe	tat Tyr 185	ggg ( Gly '	aca Thr	ggc Gly	ctt Leu	ggt Gly 190	gtg Val	tat Tyr	577
ctt agt tcc Leu Ser Ser 195	aat gca Asn Ala	tcg tcc Ser Ser	tct Ser 200	tcc Ser	tgg Trp	cgg Arg	ggc Gly	atg Met 205	gtg Val	gcc Ala	tcg Ser	625
gtc atg tac Val Met Tyr 210	act gtg Thr Val	gtc acc Val Thr 215	Pro				,					649
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Leu Ala Asp	5				10					13		
Leu Ala Asp 1	5 Ala Gln 20	Ser As:	n Ala	Ile 25	Ser	Tyr	Ala	Gly	Cys 30	Ile	Ser	
Leu Ala Asp 1  Asn Ile Glr  Gln Met Tyr 35  Thr Val Met	5 Ala Gln 20 Phe Phe	Ser As:  Met Va	n Ala l Phe 40 g Tyr	Ile 25 Gly	Ser Gly	Tyr Ile	Ala Asp	Gly Thr 45	Cys 30	Ile	Ser Leu	
Leu Ala Asp 1  Asn Ile Glr  Gln Met Tyr 35  Thr Val Met	5 Ala Gln 20 Phe Phe Ala Tyr	Ser Ass Met Va Asp Ar	n Ala l Phe 40 g Tyr	Ile 25 Gly Val	Ser Gly Ala	Tyr Ile	Ala Asp Cys	Gly Thr 45 His	Cys 30 Phe	Ile Leu	Ser Leu Tyr	
Leu Ala Asp 1  Asn Ile Glr  Gln Met Tyr 35  Thr Val Met 50  Tyr Pro Val	5 Ala Gln 20 Phe Phe Ala Tyr	Met Va Asp Ar 55 Asn Pr 70	n Ala 1 Phe 40 g Tyr o Arg	Ile 25 Gly Val	Ser Gly Ala Cys	Tyr Ile Ile Gly	Ala Asp Cys 60 Leu	Gly Thr 45 His	Cys 30 Phe Pro	Ile Leu Leu	Ser Leu Tyr Val	
Leu Ala Asp 1  Asn Ile Glr  Gln Met Tyr 35  Thr Val Met 50  Tyr Pro Val 65	5 Ala Gln 20 Phe Phe Ala Tyr I Ile Met E Leu Ser 85	Met Va  Asp Ar  55  Asn Pr  70	n Ala l Phe 40 g Tyr o Arg	Ile 25 Gly Val Leu	Ser Gly Ala Cys Leu 90	Tyr Ile Ile Gly 75	Ala Asp Cys 60 Leu Gln	Gly Thr 45 His	Cys 30 Phe Pro Val	Leu Leu Leu Leu Ty:	Ser Leu Tyr Val 80	

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Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe
   130
                                            140
Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg
                    150
Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Asn Cys Gly Ser
                165
His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
Leu Ser Ser Asn Ala Ser Ser Ser Trp Arg Gly Met Val Ala Ser
Val Met Tyr Thr Val Val Thr Pro
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                                                                      120
tgcaggattg gacaccttta tgctgaccgt gatggcctac gacaggtttg tggccatctg
                                                                      180
tcaccctctg cactacacgg tcaccatgaa ccccaggete tgtggactge tggttctgge
                                                                      240
gtcctgatca tgagtgccct gaattcttca ttgcaaagct taatggtatt gcacctttcc
                                                                      300
ttctgtgcag acttggaaat tccccacttt ttctgtgaac ttaatcaggt catccacctt
                                                                      360
acctgttctg acacttttct taatgacatg gtgatgtatt tgtcagctgt gctgctgggt
                                                                      420
gggggatgtc tcattgggat cetttactet tactetaaga tegteteete tataettgea
                                                                      480
atctcatcag ttcaggggaa gtacaaggca ttttccacct gtgcatctca cctctcggtt
                                                                      540
gtctccttat ttattgtaca atcctaggtg tgtaccttag ttctgctgca acccacagct
                                                                      600
                                                                      647
cacacgcaag tgctgcagtc tcggtgatgt acactgtggt taccccc
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<sup>&</sup>lt;213> Macaca sylvanus

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> misc\_feature

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<220 <221 <222 <223	.> C	_	(649 ict =		acto	ory r	ecep	otor									
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aac Asn	atc Ile	cag Gln	aca Thr 20	cag Gln	agc Ser	aga Arg	gtc Val	atc Ile 25	acc Thr	tat Tyr	gca Ala	ggc Gly	tgc Cys 30	atc Ile	acc Thr		97
cag Gln	atg Met	tgc Cys 35	ttt Phe	ttc Phe	ata Ile	ttc Phe	ttt Phe 40	gtg Val	gga Gly	ctg Leu	gat Asp	atc Ile 45	ttt Phe	atg Met	ctg Leu		145
acc Thr	gtg Val 50	atg Met	gcc Ala	ttt Phe	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His		193
tac Tyr 65	acg Thr	gtc Val	acc Thr	atg Met	aac Asn 70	ccc Pro	agg Arg	ctc Leu	agt Ser	999 Gly 75	ctg Leu	ctg Leu	gtt Val	ctg Leu	gcg Ala 80		241
tcc Ser	tgg Trp	atc Ile	atg Met	agt Ser 85	gcc Ala	ctg Leu	aat Asn	tcc Ser	tcg Ser 90	tta Leu	caa Gln	agc Ser	tta Leu	ata Ile 95	gtg Val		289
ctg Leu	cgg Arg	ctt Leu	tcc Ser 100	ttc Phe	tgc Cys	aca Thr	gac Asp	ttg Leu 105	gaa Glu	att Ile	ccc Pro	cac His	ttt Phe 110	ttc Phe	tgt Cys		337
gaa Glu	ctt Leu	aat Asn 115	cag Gln	gtg Val	gtc Val	cac His	ctt Leu 120	gcc Ala	tgt Cys	tct Ser	gac Asp	acc Thr 125	ttt Phe	ctt Leu	aat Asn		385
gac Asp	atg Met 130	gtg Val	atg Met	tat Tyr	ttg Leu	gca Ala 135	tct Ser	gca Ala	ctg Leu	ctg Leu	ggc Gly 140	tgt Cys	ggt Gly	ccc Pro	ctc Leu		433
tct Ser 145	Gly 333	atc Ile	ctt Leu	tat Tyr	tct Ser 150	tat Tyr	tct Ser	aag Lys	atc Ile	gtt Val 155	tcc Ser	tcc Ser	ata Ile	cgt Arg	gga Gly 160		481
atc Ile	tca Ser	tca Ser	gct Ala	cag Gln 165	GJA aaa	aag Lys	tac Tyr	agg Arg	gca Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser		529
cac His	ctc Leu	tca Ser	gtt Val 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	ggt Gly	acg Thr	ctc Leu	cta Leu	gga Gly 190	gtg Val	tac Tyr		577
ttt Phe	agt Ser	tct Ser 195	gct Ala	gca Ala	acc Thr	cgt Arg	aac Asn 200	Ser	cac His	tca Ser	agt Ser	gct Ala 205	gca Ala	gcc Ala	tcg Ser		625
		Tyr	acc Thr														649

Tyr Thr Val Thr Met Asn Pro Arg Leu Ser Gly Leu Leu Val Leu Ala

55

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Ile Val 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 100 105 110

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Cys Gly Pro Leu 130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Gly 145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Arg Ala Phe Ser Thr Cys Ala Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190

Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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cag Gln	ctc Leu	tac Tyr 35	ttc Phe	ctg Leu	gtc Val	tcc Ser	ttg Leu 40	gtg Val	gcc Ala	ctg Leu	gac Asp	aac Asn 45	ctc Leu	atc Ile	ctg Leu	145
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tac Tyr 65	acc Thr	aca Thr	gcc Ala	atg Met	agc Ser 70	cct Pro	aag Lys	ctc Leu	tgt Cys	atc Ile 75	tta Leu	ctc Leu	ctt Leu	tcc Ser	ttg Leu 80	241
tgt Cys	tgg Trp	gtc Val	tta Leu	tct Ser 85	gtg Val	ctc Leu	tat Tyr	ggc Gly	ctc Leu 90	ata Ile	cac His	acc Thr	ttc Phe	ctc Leu 95	atg Met	289
acc Thr	acg Thr	gtg Val	acc Thr 100	ttc Phe	tgt Cys	ggg ggg	tca Ser	cga Arg 105	aaa Lys	atc Ile	cac His	tac Tyr	atc Ile 110	ttc Phe	tgt Cys	337
gag Glu	atg Met	tat Tyr 115	gta Val	ttg Leu	ctg Leu	agg Arg	ctg Leu 120	gca Ala	tgt Cys	tcc Ser	gac Asp	act Thr 125	cag Gln	att Ile	aat Asn	385
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gga Gly 145	Phe	atg Met	atc Ile	att Ile	tcc Ser 150	Tyr	gtg Val	ttg Leu	att Ile	gtc Val 155	Arg	gcc Ala	atc Ile	ctc Leu	aga Arg 160	481
ata Ile	ccc Pro	tca Ser	gtc Val	tct Ser 165	Lys	aaa Lys	tac Tyr	aaa Lys	gcc Ala 170	Phe	tcc Ser	act Thr	tgt Cys	gcc Ala 175	Ser	529
cat His	ttg Leu	ggt Gly	gta Val 180	Val	tcc Ser	ctc Leu	ttc Phe	tat Tyr 185	Gly	aca Thr	ctt Leu	cgt Arg	atg Met 190	vaı	tac Tyr	577
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Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu Ser Leu
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65
Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr Phe Leu Met
Thr Thr Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr Ile Phe Cys
                                 105
            100
Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asp Thr Gln Ile Asn
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His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Phe
Gly Phe Met Ile Ile Ser Tyr Val Leu Ile Val Arg Ala Ile Leu Arg
145
Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Arg Met Val Tyr
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Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val Ala Thr Val

## Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp.Ser Val Ala Thr Val 195 200 205

Met Tyr Ala Val Val Thr Pro 210 215

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aac atc cag acc aag aac aaa acc atc tct tac atg gac tgc ctc acc Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr 20 25 30													
cag gtc tat ttc tcc atg ttt ttt cct att ctg gac acg cta ctc ctg Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu 35 40 45													
acc gtg atg gct tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac  Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His  50 55 60													
tat gta acc atc atg aac ccc cgc ctc tgc ggc ctc ctg gtt ttt gtc Tyr Val Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val 70 75 80													
acg tgg ctc att ggt gtc atg aca ccc ctc ctc cat att tct ctg ttg  Thr Trp Leu Ile Gly Val Met Thr Pro Leu Leu His Ile Ser Leu Leu  85  90  95													
acg cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys 100 105 110													
gaa ctg aca cac atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125													
agc acg ttg ata tat gtt atg aca ggt gtg ctg ggc gtt ttt ccc ctc  Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu  130 135 140													
ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys 145 150 155 160													
atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct 529													

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser 165 170 175													
cac ctc tcc atc gtt tct tta ttt tat ggg aca ggc att ggg gtc cat His Leu Ser Ile Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His 180 185 190													
ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser 195 200 205													
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His 50 60													
Tyr Val Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val 65 70 75 80													
Thr Trp Leu Ile Gly Val Met Thr Pro Leu Leu His Ile Ser Leu Leu 85 90 95													
Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys 100 105 110													
Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125													
Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu 130 135 140													
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<223> Product = olfactory receptor

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His Leu Ser Ile Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
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Val Met Tyr Thr Val Val Thr Pro
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                                                                     240
ccacccctg cactacacgg tcatcatgaa cccctgcctc tgtggcatcc tggttctggc
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cgctctgata ctctcctcgt taacattgtc ttgtatgtgg ccacagcact gctgggtgtg
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cttcctgtag ctgggatcct cttctcctac tctcagatcg tctcctcctt aatgaggatg
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tcctccaccg agggcaagta caaagccttt tccacctgtg ggtctcacct ctgtgtggtc
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tccttgttct atggaacagg acttggggtc tatctcagtt ctgctgtgac ccattcttcc
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cag atg tat ttt ttc atg Gln Met Tyr Phe Phe Met 35													
acc gtg atg gcc tat gac Thr Val Met Ala Tyr Asp 50													
tac cct gtc att atg aac Tyr Pro Val Ile Met Asn 65 70	ccc cgc ctc t Pro Arg Leu (	tgt ggc ctg ctg Cys Gly Leu Leu 75	gtt ctt gtg 241 Val Leu Val 80										
tcc tgg ttc ctc agc ttg Ser Trp Phe Leu Ser Leu 85	Ser Tyr Ser I	ctg atc cag agt Leu Ile Gln Ser 90	ctg ttg atg 289 Leu Leu Met 95										
ctg cag ttg tcc ttt tgc Leu Gln Leu Ser Phe Cys 100	acc agt tgg of Thr Ser Trp V	gtc att cag cac Val Ile Gln His	ttt tac tgc 337 Phe Tyr Cys 110										
gag ctt gct cag gcc ctc Glu Leu Ala Gln Ala Leu 115													
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tca gga atc ctt ttc tcc Ser Gly Ile Leu Phe Ser 145	Tyr Thr Gln	att gtc tcc tcc Ile Val Ser Ser 155	atc ctg aga 481 Ile Leu Arg 160										
atc tca tcc aca gat ggg Ile Ser Ser Thr Asp Gly 165	, Lys His Lys A	gcc ttt tct acc Ala Phe Ser Thr 170	tgc gga tct 529 Cys Gly Ser 175										
cat ctg tct gtg gtt ttt His Leu Ser Val Val Phe 180	tta ttc tat o Leu Phe Tyr ( 185	ggg aca ggc ctt Gly Thr Gly Leu	ggt gtg tat 577 Gly Val Tyr 190										
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Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met

Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys

Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn

Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe

Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg

Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser 165

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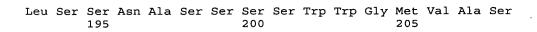
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cag Gln	ttg Leu	tac Tyr 35	ttc Phe	ttt Phe	gta Val	ctc Leu	ttc Phe 40	ata Ile	Gly 333	ttg Leu	gac Asp	agc Ser 45	tta Leu	ctc Leu	ccg Pro	145
acc Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
tac Tyr 65	acg Thr	gtc Val	atc Ile	atg Met	aac Asn 70	cct Pro	cag Gln	ttc Phe	tgt Cys	gga Gly 75	ctg Leu	ctg Leu	gtt Val	ctg Leu	gtg Val 80	241
tcc Ser	tgg Trp	atc Ile	atg Met	agt Ser 85	gcc Ala	ctg Leu	cat His	tct Ser	ttg Leu 90	aca Thr	gaa Glu	agc Ser	tta Leu	atg Met 95	gta Val	289
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gaa Glu	att Ile	cat His 115	cag Gln	ata Ile	att Ile	caa Gln	ttt Phe 120	gcc Ala	tgt Cys	tct Ser	gac Asp	acc Thr 125	ttt Phe	ctt Leu	aat Asn	385
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gct Ala 145	Gly 333	atc Ile	ctg Leu	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gct Ala 155	tcc Ser	tct Ser	ata Ile	cgt Arg	gca Ala 160	481
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cac His	ctc Leu	tca Ser	gtt Val 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	tgt Cys	aca Thr	ggc Gly	cta Leu	999 Gly 190	gtg Val	tac Tyr	577
ctg Leu	agt Ser	tct Ser 195	gct Ala	gca Ala	acc Thr	cac His	agc Ser 200	tca Ser	ctc Leu	tca Ser	agc Ser	gca Ala 205	gca Ala	gcc Ala	tcg Ser	625
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- Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 60
- Tyr Thr Val Ile Met Asn Pro Gln Phe Cys Gly Leu Leu Val Leu Val 65 70 75 80
- Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Val 85 90 95
- Tyr Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro Gln Phe Phe Cys 100 105 110
- Glu Ile His Gln Ile Ile Gln Phe Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125
- Asn Leu Val Met Tyr Leu Ser Thr Val Leu Leu Gly Gly Pro Leu 130  $$135\$
- Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala 145 150 155 160
- Ile Ser Ser Ala Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 175
- His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr 180 185 190
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aac atc cag gag cag agt ggt acc atc agc tat gca ggc tgc att gcc
                                                                       97
Asn Ile Gln Glu Gln Ser Gly Thr Ile Ser Tyr Ala Gly Cys Ile Ala
                                                                      145
cag atg tat ttt ttc atg gtt ttt gga ggc atg gac aca ttt ctc ctc
Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr Phe Leu Leu
                            40
act gtg atg gcc tat gac cgg tat gtg gct atc tgt cac ccc ctg tcc
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Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Ser
tac cct gtc att gta aac ccc cgc ctc tgc ggc ctg ttg gtt ctt gtg
                                                                      241
Tyr Pro Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
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65
                                                                      289
tcc tgg ttc ctc agc ttg tca tac tcc ctg atc cag agt ctg ttg atg
Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
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ctg cgg cta tcc ttc tgc acc agt tgg gtc att cag cac ttt tac tgt
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Leu Arg Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
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                                                                      385
gag oft got cag git oft acg oft god tgo toa gad aca cat git aat
Glu Leu Ala Gln Val Leu Thr Leu Ala Cys Ser Asp Thr His Val Asn
                            120
                                                 125
                                                                      433
tac atc ctg ctc tac atg gtg acc ggc ctt ctg ggc tgt gtt ccc ttc
Tyr Ile Leu Leu Tyr Met Val Thr Gly Leu Leu Gly Cys Val Pro Phe
tca ggg atc ctt ttc tcc tac atc caa att gtc tcc tcc atc ctg aga
                                                                      481
Ser Gly Ile Leu Phe Ser Tyr Ile Gln Ile Val Ser Ser Ile Leu Arg
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                                                             160
145
atc cca tcc aca gat ggg aaa cat aaa gcc ttt tct acc tgt gga tct
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Ile Pro Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser
cat ctg tct gtg gtt tct tta ttc tac ggg aca ggc ctt ggt gtc tac
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His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
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Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr Phe Leu Leu 35 40 45													
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Ser 50 55 60													
Tyr Pro Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val 65 70 75 80													
Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met 85 90 95													
Leu Arg Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys 100 105 110													
Glu Leu Ala Gln Val Leu Thr Leu Ala Cys Ser Asp Thr His Val Asn 115 120 125													
Tyr Ile Leu Leu Tyr Met Val Thr Gly Leu Leu Gly Cys Val Pro Phe 130 135 140													
Ser Gly Ile Leu Phe Ser Tyr Ile Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160													
Ile Pro Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175													
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		tac Tyr 35														145
		atg Met														193
		gtg Val														241
		agc Ser														289
		ctg Leu														337
		cag Gln 115		Val	Leu		Leu	Ser		Ser	Asp					385
		gtg Val														433
		atc Ile														481

atc ccc ttt gca gct ggg aag tgg agg gcc ttc tct acc tgt ggc tcc  Ile Pro Phe Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser  165 170 175	)												
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Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp Ser Tyr Leu Leu 35 40 45													
Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His 50 55 60													
Tyr Asp Val Ala Met Asn Pro Arg His Cys Leu Leu Met Leu Gly 65 70 75 80													
Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met 85 90 95													
Ser His Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys 100 105 110													
Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser 115 120 125													
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Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg 145 150 155 160													

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Ile Pro Phe Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser
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His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Tyr Tyr Val Tyr
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aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc
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Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
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                                 25
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Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu
act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac cca ctg cac
                                                                         193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
                         55
                                                                         241
tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca
Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg
                                                                         289
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
                                      90
                85
                                                                         337
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Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
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gaa ctt aat cag gtc atc cac ctt gcc tgt tct gac act ttt ctt aat Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

gat gtg gtg atg tat ttg gcc gct gtg ctg ctg ggg ggt ggt ccc ctt Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Pro Leu 130 135 140	433											
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atc tca tca gct cag ggg aag tac aag gca ttt tcc acc tgt gta tct  Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser  165 170 175	529											
cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190	577											
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Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 10												
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 1 Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 20 Leu Phe Ala Val Leu Asp Val Phe Met Leu 40 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His												
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 15  Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 25  Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu 40  Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50  Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala												
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 15  Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 20  Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu 40  Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 60  Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 80  Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val												

Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Pro Leu 130 135 140												
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160												
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His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190												
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Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Cys 100 105 110	337											
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aaa atc gtg atg tat ttt gtg aca att gca atg ggt gtt ttt cct ctc Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu 130 135 140	433											
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Asp '	<b>V</b> al	Leu 115	Glu	Val	Leu	Lys	Leu 120	Ala	Cys	Ser	Glu	Thr 125	Leu	Val	Asn	
 Lys :	Ile 130	Val	Met	Tyr	Phe	Val 135	Thr	Ile	Ala	Met	Gly 140	Val	Phe	Pro	Leu	
Ser (	Gly	Ile	Leu	Tyr	Ser 150	Tyr	Ser	Gln	Ile	Phe 155	Ser	Ser	Ile	Leu	Arg 160	
Val s	Ser	Pro	Ala	Gln 165	Gly	Gln	His	Lys	Ala 170	Phe	Ser	Thr	Cys	Gly 175	Ser	
His 1	Leu	Ser	Val 180	Val	Thr	Leu	Phe	Tyr 185	Gly	Thr	Gly	Leu	Gly 190	Val	Tyr	
Leu S	Ser	Leu 195	Ala	Ala	Thr	Pro	Ser 200	Ser	Arg	Thr	Ser	Leu 205	Met	Ala	Ser	
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aac a Asn :																97
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gct q Ala																193

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gac cct tct caa ctc ctc aca ctt gct tgt tcc gac acg ttt gtc aat Asp Pro Ser Gln Leu Leu Thr Leu Ala Cys Ser Asp Thr Phe Val Asn 115 120 125	385 ·												
aac aac ata gtc atg aat ttc ttt gct gct gta ttt ggt ttt ctt ccc Asn Asn Ile Val Met Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro 130 135 140	433												
atc tca ggg atc ttt ttg tct tac tat aaa att gtt tcc tcc att ctg Ile Ser Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu 145 150 155 160	481												
aga gtt cca tca tca agt ggg aag tat aaa gcc ttc tct acc tgt agc Arg Val Pro Ser Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser 165 170 175	529												
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Ser Ala Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
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Leu Gln Phe Ser Cys Phe Lys Asp Ile Lys Ile Ser Asn Phe Phe Cys
                                105
Asp Pro Ser Gln Leu Leu Thr Leu Ala Cys Ser Asp Thr Phe Val Asn
Asn Asn Ile Val Met Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro
Ile Ser Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
                                        155
Arg Val Pro Ser Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser
                                    170
Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Leu Gly Val
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Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
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25

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ctg Leu	cgg Arg	ctt Leu	tcc Ser 100	ttc Phe	tgc Cys	aca Thr	gac Asp	ttg Leu 105	gaa Glu	atc Ile	ccc Pro	cac His	ttt Phe 110	ttc Phe	tgc Cys		337
gta Val	ctt Leu	aat Asn 115	cag Gln	gtc Val	atc Ile	cac His	ctt Leu 120	gcc Ala	tgt Cys	tct Ser	gac Asp	act Thr 125	ttt Phe	ctt Leu	aat Asn		385
gat Asp	gtg Val 130	gtg Val	atg Met	tat Tyr	ttg Leu	gcc Ala 135	gct Ala	gtg Val	ctg Leu	ctg Leu	999 Gly 140	ggt Gly	ggt Gly	ccc Pro	ctt Leu		433
gca Ala 145	gly ggg	att Ile	ctt Leu	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gtt Val 155	tcc Ser	tcc Ser	ata Ile	cgt Arg	gca Ala 160		481
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cac His	atc Ile	tta Leu	att Ile 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	ggt Gly	aca Thr	ctc Leu	cta Leu	ggt Gly 190	gtg Val	tac Tyr	!	577
ctt Leu	Ser	tct Ser 195	gct Ala	gca Ala	act Thr	Gly .	aac Asn 200	tca Ser	cat His	tca Ser	aga Arg	gct Ala 205	gca Ala	gcc Ala	tcg Ser	•	525
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Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu 35 4.0

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Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys

Val Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120

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Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 170 165

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aat ttt cta tca gag aca aag gtt atc tcc tac atg ggc tgc ctg gtc Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Met Gly Cys Leu Val 20 25 30	97
cca atg tac ttc ttc atg gcc ttt gcg aac act gac agc tac ctg ctg Pro Met Tyr Phe Phe Met Ala Phe Ala Asn Thr Asp Ser Tyr Leu Leu 35 40 45	145
gcc tct atg gcc atc gac cgg ctg gtg gcc atc tgc aac ccc tta cac Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His 50 55 60	193
tat gat gtg gct atg aac tcc cgg cgt tgc cta ctc atg cta ttg ggt Tyr Asp Val Ala Met Asn Ser Arg Arg Cys Leu Leu Met Leu Leu Gly 65 70 75 80	241
tct tgc agc atc tcc cac cta cat tcc ctg ttc cgg gtg cta ctt atg Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met 85 90 95	289
tct cgc ctg tct ttc tgt gcc tcc cac gtc att aag cac ttt ttc tgt Ser Arg Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys 100 105 110	337
gac acc cag cct gtg cta aag ctg tcc tgc tct gac acg tcc tcc agc Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser 115 120 125	385
cag atg gtg gtc atg act gag acc tta gct gtt att gtg acc ccc ttc Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe 130 135 140	433
ctg tgt atc atc ttc tcc tac ctg cga atc atc atc act gtg ctc aga Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg 145 150 155 160	481
atc ccc tct gca gcc ggg aag tgg agg gcc ttc tct acc tgt ggc tcc Ile Pro Ser Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser 165 170 175	529
cac ctc act gta gta gcc ctt ttc tac ggg agt att att tat gtc tat His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr 180 185 190	577
ttt agg ccc ctg tcc atg tac tca gtg gtg aag gac cga gta gcc aca Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr 195 200 205	625
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Pro Met Tyr Phe Phe Met Ala Phe Ala Asn Thr Asp Ser Tyr Leu Leu 35 40

Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His 50 55 60

Tyr Asp Val Ala Met Asn Ser Arg Arg Cys Leu Leu Met Leu Leu Gly 65 70 75 80

Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met 85 90 95

Ser Arg Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Cys 100 105 110

Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser 115 120 125

Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe 130 140

Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg 145 150 155 160

Ile Pro Ser Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr 180 185 190

Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 107

<211> 649

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc\_feature

<222> (1)..(649)

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cag Gln	att Ile	ttt Phe 35	ttt Phe	ttc Phe	gtt Val	gca Ala	ttt Phe 40	gga Gly	tgc Cys	ctg Leu	gac Asp	aat Asn 45	ttg Leu	ctc	ttg Leu	145
acc Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttc Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac	193
tac Tyr 65	gcg Ala	gtc Val	atc Ile	atg Met	aac Asn 70	ccc Pro	cgg Arg	ctc Leu	tgt Cys	aga Arg 75	ctg Leu	cta Leu	gtt Val	ctg Leu	80 Gly 333	241
tcc Ser	tgg Trp	tgc Cys	atc Ile	agt Ser 85	gtc Val	atg Met	gtt Val	tct Ser	ctg Leu 90	ctc Leu	gag Glu	acc Thr	ttg Leu	acc Thr 95	att Ile	289
ttg Leu	agg Arg	ctg Leu	tcc Ser 100	ttc Phe	tgc Cys	aca Thr	aac Asn	atg Met 105	gaa Glu	atc Ile	cca Pro	cac His	ttt Phe 110	ttt Phe	tgt Cys	337
gat Asp	gtt Val	ctc Leu 115	gaa Glu	gtc Val	ctg Leu	aag Lys	ctc Leu 120	gcc Ala	tgt Cys	tct Ser	gaa Glu	acc Thr 125	ctc Leu	gtc Val	aat Asn	385
aaa Lys	atc Ile 130	gtg Val	atg Met	tat Tyr	ttt Phe	gtg Val 135	aca Thr	att Ile	gca Ala	atg Met	ggt Gly 140	gtt Val	ttt Phe	cct Pro	ctc Leu	433
tct Ser 145	gga Gly	atc Ile	cta Leu	tac Tyr	tct Ser 150	tat Tyr	tct Ser	cag Gln	att Ile	ttc Phe 155	tcc Ser	tcc Ser	atc Ile	ctg Leu	aga Arg 160	481
gta Val	tca Ser	cct Pro	gcc Ala	caa Gln 165	ggc Gly	cag Gln	cac His	aaa Lys	gcc Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	999 Gly 175	tct Ser	529
cac His	ctc Leu	tca Ser	gtg Val 180	gtc Val	acc Thr	ctg Leu	ttc Phe	tat Tyr 185	ggc Gly	acg Thr	ggc Gly	ctt Leu	999 Gly 190	gta Val	tat Tyr	577
ctc Leu	agt Ser	tct Ser 195	gca Ala	gct Ala	aca Thr	cca Pro	tct Ser 200	tct Ser	agg Arg	aca Thr	agt Ser	ctg Leu 205	atg Met	gcc Ala	tcg Ser	625
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- Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu
- Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
- Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly 75
- Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile
- Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Cys 105
- Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn 120
- Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu 135
- Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg 150
- Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
- His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
- Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser 195
- Val Met Tyr Thr Met Val Thr Pro 210 215

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													ttg Leu			145
													ccc Pro			193
													gtt Val			241
													ttg Leu			289
													ttt Phe 110			337
													ctc Leu			385
													ttt Phe			433
													atc Ile			481
													tgt Cys			529
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195 200 205

gtg atg tac acc atg gtc acc ccc
Val Met Tyr Thr Met Val Thr Pro

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Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly 65 70 75 80

Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Cys
100 105 110

Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn 115 120 125

Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu 130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg 145 150 155 160

Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 190

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AF127885
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cctgtcaccc tctgtatcat tcagccatca tgaagtcatg tttctgtggc tttctagttt
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                                                                         300
gcaaatggcc tgctttgagg atgtggaaat ttctaatttc ttctgtgacc cttctcaact
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                                                                         420
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cattetgagg getteateat caggtgggag gtataaagee ttetecatet gtgggtetea
                                                                         540
cctgtcagtt gtttgcttat tttatggaac aggcatatgg gggtacctca gttcagatgt
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  1
                   5
                                        10
gac atg caa act cac age aga gtc atc tcc tat gca ggc tgc ctg act
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Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
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Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser

195

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agt gtg atg g Ser Val Met A 50	gcc tat gac Ala Tyr Asp	cgg ttt gtg Arg Phe Val	g gcc atc tgt l Ala Ile Cys 60	cac cct ccg His Pro Pro	gat 193 Asp
tac cca gtt a Tyr Pro Val T 65	acc atg aac Thr Met Asn 70	cca tgt tto Pro Cys Phe	c tgt ggc ttc e Cys Gly Phe 75	cta gtt ttg Leu Val Leu	ttg 241 Leu 80
tct ttt ttt c Ser Phe Phe L	etc agt ctt Leu Ser Leu 85	tta gac tco Leu Asp Sei	c cag ctg cac r Gln Leu His 90	aat tgg att Asn Trp Ile 95	gcc 289 Ala
tta caa att a Leu Gln Ile T 1	acc tgc ttc Thr Cys Phe .00	aag gat gtg Lys Asp Val	l Glu Ile Pro	aat ttc ttc Asn Phe Phe 110	tgt 337 Cys
gac cct tcc c Asp Pro Ser G 115					
gac ata gtc a Asp Ile Val M 130				Phe Leu Pro	
ttg ggg atc c Leu Gly Ile L 145					
gtt tca tca t Val Ser Ser S					
cac ctg tca g His Leu Ser V 1			r Gly Thr Ala		
ctc agt tca g Leu Ser Ser A 195					
gtg atg tac a Val Met Tyr T 210					649
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Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr

Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp Asp Met Leu Leu

Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Pro Asp

Tyr Pro Val Thr Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu Leu

Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile Ala 85 90

Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys 100 105

Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn

Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro Ile

Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu Arg

Val Ser Ser Ser Gly Gly Arg Tyr Lys Ala Phe Ala Thr Cys Gly Ser 165

His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Ala Leu Gly Gly Tyr

Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala Ser

Val Met Tyr Thr Val Val Thr Pro

<210> 114

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<212> DNA

<213> Pongo pygmaeus

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ggcacggaag agagacatgc teetgagtgt gatggeetat gaccggtttg tagecatetg
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                                                                        300
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                                                                       360
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                                                                       420
 tttgcttttc ttcccatctc ggggactctt ttctcttact ctaatattgt ctcctccatt
                                                                       480
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                                                                       540
 tcagttgttt gctgagcttc tggaacaggc gttggagggt acctcagttc agatgtgtca
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                                       10
aac atc cag gca cgg agc aaa gaa atc tcc tac atg ggg tgc ctc act
                                                                        97
Asn Ile Gln Ala Arg Ser Lys Glu Ile Ser Tyr Met Gly Cys Leu Thr
                                 25
cag gtg tat ttt tta atg atg ttt gct gga atg gat act ttc cta ctg
                                                                       145
Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
                            40
gct gtg atg gct tat gac cgg ttt gtg gcc atc tgc cac ccc ctt cag
                                                                       193
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Gln
    5.0
tac gcg gtc atc atg aac ccc cat ctc tgt ggc ctg ctg gtt ctg gca
                                                                      241
Tyr Ala Val Ile Met Asn Pro His Leu Cys Gly Leu Leu Val Leu Ala
tet tgg tte ate att tte tgg gte tee etg gtt cat att eta etg atg
                                                                      289
Ser Trp Phe Ile Ile Phe Trp Val Ser Leu Val His Ile Leu Leu Met
aag agg ctg acc ttc tcc aca ggc act gag att ccg cat ttc ttc tgt
                                                                      337
Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
                                105
gaa ctg gct cag gtc ctc aag gtg gcc cgc tct gat acc ctc ctc aat
                                                                      385
Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Thr Leu Leu Asn
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115 120 125

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	gct Ala 145	gjà aaa	atc Ile	ctc Leu	ttc Phe	tcc Ser 150	tac Tyr	tct Ser	cag Gln	atc Ile	gtc Val 155	Ser	tcc Ser	tta Leu	atg Met	aga Arg 160	481	
													acc Thr				529	
	cac His	ctc Leu	tgt Cys	gtg Val 180	gtc Val	tcc Ser	ttg Leu	ttc Phe	aat Asn 185	Gly	aca Thr	gga Gly	ctt Leu	999 Gly 190	gtc Val	tat Tyr	577	
	ctc Leu	agt Ser	tct Ser 195	gct Ala	gtg Val	acc Thr	cat His	tct Ser 200	tcc Ser	cag Gln	agc Ser	agc Ser	tcc Ser 205	atg Met	gcc Ala	tca Ser	625	
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(	3ln	Val	Tyr 35	Phe	Leu	Met	Met	Phe 40	Ala	Gly	Met	Asp	Thr 45	Phe	Leu	Leu		
1		Val 50	Met	Ala	Tyr	Asp	Arg 55	Phe	Val	Ala	Ile	Cys 60	His	Pro	Leu	Gln		
6	Tyr . 55	Ala	Val	Ile	Met	Asn 70	Pro	His	Leu	Cys	Gly 75	Leu	Leu	Val	Leu	Ala 80		
5	Ser '	Trp	Phe		Ile 85	Phe	Trp	Val	Ser	Leu 90	Val	His	Ile	Leu	Leu 95	Met		

Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys 100 105 110

Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Thr Leu Leu Asn 115 120 125

Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val 130 135 140

Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Cys Val Val Ser Leu Phe Asn Gly Thr Gly Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser 195 200 205

Val Met Tyr Ala Met Val Thr Pro 210 215

<210> 117

<211> 659

<212> DNA

<213> Pongo pygmaeus

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= AF127889

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<sup>&</sup>lt;211> 648

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= AF127890
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                                                                     120
                                                                     180
tgcaggattg gacatctttc tcctgactgt gatggcctat gacggtttgt ggccatctgt
                                                                     240
cacccctgc actacacggt catcatgagc cccaggctct gtggactgct ggttctggca
tectggatea tgagtgeest gaatteettg etacaaaget taatagtast geggetttee
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                                                                     360
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gcctgttctg acacctttct taacgacatg gtgatgtatt tgtcatctgc gttgtggggc
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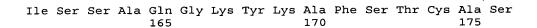
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gat Asp	gtg Val 130	gtg Val	atg Met	tat Tyr	ttg Leu	gca Ala 135	gct Ala	atg Met	ctg Leu	ctg Leu	ggc Gly 140	ggt Gly	ggt Gly	ccc Pro	ctc Leu		433
aca Thr 145	gga Gly	att Ile	att Ile	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gtt Val 155	tcc Ser	tcc Ser	ata Ile	cgt Arg	gca Ala 160		481
atc Ile	tca Ser	tca Ser	gct Ala	cag Gln 165	gjå aaa	aag Lys	tac Tyr	aag Lys	gcg Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser		529
cac His	atc Ile	tta Leu	att Ile 180	gtc Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	ggt Gly	aca Thr	ctc Leu	cta Leu	ggt Gly 190	gtg Val	tac Tyr		577
ctt Leu	agt Ser	tct Ser 195	gct Ala	gca Ala	act Thr	Gly	aac Asn 200	tca Ser	cat His	tca Ser	ggt Gly	gct Ala 205	gca Ala	gcc Ala	ttg Leu		625
Val	atg Met 210	tac Tyr	act (	gtg Val	Val	acc Thr 215	ccc Pro										649
<210 <211 <212 <213	> 2 > P	31 16 RT aimi:	ri bo	oliv	iens	is											
<220 <221 <222 <223	> m: > (:	1)	featı (649) = 27		; gei	ne =	SBO	29; .	Acce	ssio:	n DD	BJ/EI	MBL/	GenBa	ank =	: AF1	27899
<400: Phe 1		31 Asp I	Ile C	Cys 1	Phe '	Val S	Ser :		Thr '	Val :	Pro :	Lys 1		Leu ' 15	Val		
Asn I	Ile (	∃ln 7	Thr H 20	lis S	Ser I	iys V	/al [	[le :	Thr 1	Phe 1	Ala (		Cys I	Ile 7	Thr		
Gln 1	[le 6	Ely H	His C	ys I	Leu I	Leu F	he A	Ala <i>P</i>	Ala I	Leu <i>I</i>		Ile I 15	Phe N	Met I	Leu		
Thr V	al M	let A	Ala T	yr A	sp A	rg T	'yr V	al A	Ala I		Cys F	lis F	ro I	eu H	His		

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Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Arg Phe Phe Cys
Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
                                        155
                    150
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
                165
                                    170
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Gly Ala Ala Ala Leu
Val Met Tyr Thr Val Val Thr Pro
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aat atc cag aca cac agc aaa gtc atc acc ttt gca gac tgc atc acc
Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Asp Cys Ile Thr
                                                                     145
cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg
Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
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40 45 35 193 act gtg atg gcc tat gac cgg tat gtg gcc acc tgt cac ccc ctg cac Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys His Pro Leu His tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca 241 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa ccc tta ata gtg 289 Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val 85 ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc 337 Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 100 105 110 gaa ctt aat cag gtc ata cat ctt gcc tgt tat gac act ttc ctt aat 385 Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 115 120 gat gtg gtg atg tat ttg gca gct atg ctg ctg ggc ggt ggt ccc ctc 433 Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu 135 aca gga att att tac tct tac tct aag ata gtt tcc tcc ata cgt gca 481 Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 150 155 atc tca tca gct cag ggg aag tac aag gcg ttt tcc acc tgt gca tct 529 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac 577 His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 ctt agt tct gct gca act ggc aac tca cat tca agt gct gca gcc ttg 625 Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 200 gtg atg tac aca gtg gtc acc ccc Val Met Tyr Thr Val Val Thr Pro 649 <210> 133 <211> 216 <212> PRT <213> Saimiri boliviensis <220> misc\_feature (1)..(649) <222> Taxon = 27679; gene = SBO30; Accession DDBJ/EMBL/GenBank = AF127900

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Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Asp Cys Ile Thr 20 30

- Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
- Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys His Pro Leu His
- Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
- Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val
- Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Cys 105 100
- Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 120
- Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
- Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 150
- Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
- His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 185
- Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 200
- Val Met Tyr Thr Val Val Thr Pro 210
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- <223> Product = olfactory receptor
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<400> 135

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Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
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- Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
- Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu 40
- Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
- Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
- Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val 90
- Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 105
- Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 125
- Asp Val Val Met Tyr Leu Ala Ala Met Leu Gly Gly Gly Pro Leu
- Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
- Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170
- His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 185
- Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 195
- Val Met His Thr Val Val Thr Pro 210 215
- <210> 136 <211> 646
- <212> DNA
- <213> Saimiri sciureus
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aac att caa act cac agc aga gtc atc gcc tat gcg agc tgc ctg aca Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr 20 25 30	97
cag gtg tct ttt tca atc ttt ttt gcg tgt atg gaa gac acg ctc ctg Gln Val Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu 35 40 45	145
gct gtg atg gcc tat gac cgg ttt gtt gcc atc tgt cac ccc ctg cac Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60	193
tac cca gtc atc atg aac cca cga ctc tgt ggc ttc tta gtg ttg gtg Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val 65 70 75 80	241
tct gtt ttt ctt agc ctt tta ata tcc cag gtg cac aat ttg att gtc Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 90 95	289
tta caa ttt tct tgc ttc aaa gag ata aag att tct aat ttc ttc tgt Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys 100 105 110	337
gac cct tct caa ctc ctc acc ctt tct tgt tct gac acc ttt gtc aat Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn 115 120 125	385
aac ata gtc acg aat ttc ttt gct gct gta ttt ggt ttt ctt ccc atc Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 130 135 140	133
tca ggg atc ttt ttc tct tac tat aaa att gcc tcc tcc att ctg aga Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg 145 150 160	181
gtt cca tta tca agt ggg aag tat aaa gcc ttc tcc acc tgt agc tct Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175	529
cac ctg gca gtt gtt tgc tta ttt tat gga aca gtt att gga gtg tac His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr 180 185 190	577
ctt ggg tca tca atg gca tcc ccc agg aag agt gtg gtg gcc tca gtg Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val 195 200 205	525
atg tac aca gtg gtc act ccc  Met Tyr Thr Val Val Thr Pro 210 215	546
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Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr 20 25 30

Gln Val Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu 35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val 65 70 75 80

Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 90 95

Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys
100 105 110

Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn 115 120 125

Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 130 135 140

Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg . 145 150 155 160

Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175

His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr 180 185 190

Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val 195 200 205

Met Tyr Thr Val Val Thr Pro 210 215

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                                      10
aac atg cag age caa gac eca tee ate eee tat geg gge tge etg ace
                                                                       97
Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
cag atg tac ttc ttc ttg tat ttt tcg gat cta gag agc ttc ctc ctt
                                                                      145
Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser Phe Leu Leu
gtg gcc atg gcc tat gac cgc tac gtg gcc atc tgc ctc ccc cta cat
                                                                      193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His
                        55
                                            60
tac gcc acc atg agc ccc atg ctg tct cgc tcc ctg gtg gcg ctg
                                                                      241
Tyr Ala Thr Ile Met Ser Pro Met Leu Ser Arg Ser Leu Val Ala Leu
                    70
tcc tgg gtg ctg acc acc ttc cat gcc atg ttg cac act tta ctc atg
                                                                      289
Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
gcc agg ttg cgt ttt tgt gca gac aat gtg atc ctc cac ttt ttc tgt
                                                                      337
Ala Arg Leu Arg Phe Cys Ala Asp Asn Val Ile Leu His Phe Phe Cys
            100
                                105
gat atg tct gct ctg ctg aag ctg gcc tgc tct gac act cga gtt aat
                                                                      385
Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn
        115
                            120
                                                125
gaa ttg gtg ata ttt atc atg gga ggc ctc att ctt gtc atc cca ctt
                                                                      433
Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Leu
                        135
cta ctt atc att ggg tcc tac gca cga att gtc ttc tcc atc ctc aag
                                                                      481
Leu Leu Ile Ile Gly Ser Tyr Ala Arg Ile Val Phe Ser Ile Leu Lys
gte cet tet tet aag ggt ate tge aag gee gte tet aet tgt gge tee
                                                                      529
Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Val Ser Thr Cys Gly Ser
                165
                                    170
cac ctc tct gtg gtg tca ctg ttc tat ggg act gtt att ggt ctc tac
                                                                      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr
tta tgc cca tca gct aat aat tct act cta aag gag act gtc atg gct
                                                                      625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Glu Thr Val Met Ala
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Val Met Tyr Thr Val Met Ala Pro
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<213> Saimiri sciureus

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Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser Phe Leu Leu 35 40

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His

Tyr Ala Thr Ile Met Ser Pro Met Leu Ser Arg Ser Leu Val Ala Leu

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met 90

Ala Arg Leu Arg Phe Cys Ala Asp Asn Val Ile Leu His Phe Phe Cys

Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn 120

Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Leu 130

Leu Leu Ile Ile Gly Ser Tyr Ala Arg Ile Val Phe Ser Ile Leu Lys 145 150 155 160

Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Val Ser Thr Cys Gly Ser 165 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Glu Thr Val Met Ala 195 200

## Val Met Tyr Thr Val Met Ala Pro 210 215

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aac att Asn Ile															97
cag ato															145
gct gtg Ala Val 50															193
tac cca Tyr Pro 65															241
tct gtt Ser Val			_					_				_		_	289
tta caa Leu Glr															337
gac cct Asp Pro		Gln	Leu	Leu	Thr	Leu	Ser	Cys	Ser		Thr	Phe			385
aac ata Asn Ile 130	val														433
tca ggg Ser Gly 145															481
gtt cca Val Pro															529

cac ctg gca gtt gtt tgc tta ttt tat gga aca gtc att gga gtg tac His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr 180 185 190
ctt ggg tca tca atg gca tcc ccc agg aag agt gtg gtg gcc tca gtg Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val 195 200 205
atg tac aca gtg gtc act ccc  Met Tyr Thr Val Val Thr Pro 210 215
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Gln Met Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu 35 40 45
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60
Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val 65 70 75 80
Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 90 95
Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys 100 105 110
Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn 115 120 125
Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 130 135 140
Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg 145 150 155 160
Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175

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His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
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Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val
        195
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Met Tyr Thr Val Val Thr Pro
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= AF127905
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tgtggtgaca gaaatattca tgctggcagt gatggcctat gacagatttg tggtggtgtg
                                                                     180
ttaccetetg ctctacacag ttgcaatgte ccagaggett ttctttttgt tagtggctac
                                                                     240
atcatacttc agggtgacag tctgtttctt gacaattacc ttctttctcc tggaattatc
                                                                     300
cttcaqaqqa aataatatca ttaataactt tqtqtqtqaq cctqctqcca ttqttqctqt
                                                                     360
gccatgcttt gacccctaca tgagccagga aatcattttc atttctgcca cattcaatga
                                                                     420
aacaagcagc ctgatgatca ttctcacctc ctaagatttc gtttttatca atgtcatgat
                                                                     480
gatgccttcc actgggggc gcataaaagc atgcgcgacc tgttcctccc agctgaccgc
                                                                     540
cattatcatt ttccatggga ccatctcttt tctctattgt gttcctaact ccaaaagttc
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<223> Product = olfactory receptor

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<400> 143

Ph 1	ne Va	al As	sp I	le Cy 5	ys Va	al Th	nr Se	er Tl	nr Th		le P	ro Ly	ys Tl	or Le	eu Se:	r	
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				tct Ser													145
		_	_	tat Tyr	_	_			_		_			_	_		193
				atg Met													241
			_	agt Ser 85	_	_			_		_	_		_	_		289
				ttt Phe													337
_			_	ata Ile				_	_		-		_				385
				tat Tyr													433
_			_	tac Tyr				_		_			_	_			481
				aag Lys 165													529
cac His			_	gtc Val					_								577
ctg Leu				gca Ala													625
gtg Val																	649
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Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr 20 25 30

Gln Leu Tyr Phe Ser Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg 50 55 60

Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Val 65 70 75 80

Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Ala 85 90 95

Leu Ser Leu Leu Phe Cys Thr Asp Leu Lys Ile Leu His Phe Cys 100 105 110

Glu Leu Asn Gln Ile Ile His Ile Ala Cys Ser Asp Thr Cys Leu Asn 115 120 125

Asn Leu Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Pro Leu 130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala 145 150 155 160

Ile Ser Ser Ala Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr 180 185 190

Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Ser Thr Ala Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro

<210> 145

<211> 649

<212> DNA

<213> Saimiri sciureus

<220>

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<222> (1)..(649)

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					agc Ser											97
					cta Leu											145
act Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
					aac Asn 70											241
					gcc Ala											289
					tgc Cys											337
					ata Ile											385
					ttg Leu											433
					tct Ser 150											481
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<220>

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Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val 85 90

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 105.

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 115

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Pro Leu

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Ala Tyr 180 185

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 200 195

Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 147

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		ctc Leu														97
gcc Ala	atg Met	tta Leu 35	cac His	act Thr	tta Leu	ctc Leu	atg Met 40	gcc Ala	agg Arg	ttg Leu	tgt Cys	ttt Phe 45	tgt Cys	gca Ala	gac Asp	145
		atc Ile														193
gcc Ala 65	tgc Cys	tct Ser	gac Asp	act Thr	cga Arg 70	gtc Val	aat Asn	gaa Glu	ttg Leu	gtg Val 75	ata Ile	ttt Phe	atc Ile	atg Met	gga Gly 80	241
		att Ile														289
cgg Arg	att Ile	gtc Val	tcc Ser 100	tcc Ser	atc Ile	ctc Leu	aag Lys	gtc Val 105	cct Pro	tcg Ser	tct Ser	aag Lys	ggt Gly 110	atc Ile	tgc Cys	337
		ttc Phe 115														385
		acc Thr														433
		aag Lys														481
_	ctg Leu															487

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<400> 149

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Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
Asn Val Ile Pro His Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
            100
                                105
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
        115
                            120
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
                                        155
Met Leu
<210> 149
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Val Ala 1 1	le Cys G 5		eu His T	yr Ser T 10	hr Leu L		ro Trp 5	
gcc tgc ato Ala Cys Met								97
gcc acc acc Ala Thr Thr 35						_	_	<b>.</b> 5
cca atc atc Pro Ile Ile 50				_	_		_	13
gca agt gct Ala Ser Ala 65								:1
gta gtc ttc Val Val Phe								19
cgc atc ctg Arg Ile Lev				-	_		_	7
aag gtc ttc Lys Val Phe 115	Ser Thr	_		_				5
ttt gga aca Phe Gly Thr 130								3
gtt acc aca Val Thr Thr 145								1
atg ct Met							48	6
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Ala Cys Met	Ala Met 20	Val Gly	Thr Ser 25	Trp Leu	Thr Gly	Ile Ile 30	Thr	
Ala Thr Thr	His Ala	Phe Leu	Ile Phe 40	Ser Leu	Pro Phe 45	Pro Ser	Arg	

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Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile
Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg
                                105
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
        115
                            120
                                                125
Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
Val Thr Thr Asp Arg Val Leu Ser Val Phe Tyr Thr Val Ile Thr Pro
                    150
                                        155
Met
<210> 151
<211> 487
<212> DNA
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= 179718
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actggctgct gcttcctggt tcccaggctt tcctgtagct actgtgcaga ccacgtggct
                                                                     120
cttcagcttt ccattctgtg gcaccaacaa ggtgaaccac ttcttctgtg acagcccacc
                                                                     180
tgtgctgaag ctggtctgtg tagacacagc actgtttgag atctacacca tcactggaac
                                                                     240
                                                                     300
cattetggtg gtcatgatcc cetgettget gatettgtgt tectacacte teattgetge
tgccatcctc aagatcccat cagctaaagg gaagcataaa gccttctcta cgtgatcctc
                                                                     360
acatctcctt gttgtctctc ttttctatct atcattaaac ctcacatatt ttcagcctaa
                                                                     420
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<210> 152 <211> 482

catgttg

487

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                                                                      120
gaccagggtg accttctgtg ggactcaaga gatccactac ctcttctgtg agatgtacgt
                                                                      180
cetgetgeag etggeatgtt ceaacacca catcattcac acagtgetgg ttgctactgg
                                                                      240
ctgctttctt cctcgacccc ttagggttca cgactacatc ctatatacgt attgtcagaa
                                                                      300
ccatccttca gataccctca gcctctaaga aacacaaaac cttctctgcc tgtgcctcac
                                                                      360
atttgggtgt ggtctccctc ttttatggga cacttgttat ggtatacctg cagccctcc
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acacctactc catgaaggac tcagtagcca cagtgatgta tgctgtggtg acacctatga
                                                                      480
                                                                      482
tq
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<223>
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                                                                       49
 Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg
tta tgc aca gtc ctt gtg gct gga gct tgg gtc gcc ggc tcc att cat
                                                                       97
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His
ggg tet ate eag gee ace etg ace tte ege eta ece tat tgt ggg ece
                                                                      145
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
                            40
aat cag gta gat tac ttt atc tgt gac atc cct gca gta ttg aga ctg
                                                                      193
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
                        55
                                            60
gcc tgt gct gac aca act gtc aat gag ctt gtg acc ttt gtg gac atc
                                                                      241
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile
65
                    70
                                        75
gga gta gtg gcc gcc agt tgc ttc atg tta att cta ctt tcc tat gcc
                                                                      289
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Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala 85 90 95
aac ata gtc cat gcc atc ctg aag ata cgc acc act gat ggg agg cgc 337 Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg 100 105 110
cgg gcc ttc tct acc tgt ggc tcc cac cta act gtg gtc aca gtc tac  Arg Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Thr Val Tyr  115 120 125
tat gtt ccc tgt att ttc atc tac ctt agg gct ggc tcc aag agc ccc 433 Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Ser Pro 130 135 140
ctg gat ggg gca gtg gct gtg ttt tac act gtt gtc act cca ttc ctg Leu Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Phe Leu 145 150 155 160
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<pre>&lt;400&gt; 154 Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg 1</pre>
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His 20 25 30
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu 50 60
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile 65 70 75 80
Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala 85 90 95
Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg 100 105 110
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Thr Val Tyr 115 120 125
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Ser Pro 130 135 140

Leu Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Phe Leu 145 150 155 160	
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ctg tgc atc cgg cta tta gtc ttg tca ttt gta ggt ggc ttc ctt cat Leu Cys Ile Arg Leu Leu Val Leu Ser Phe Val Gly Gly Phe Leu His 20 25 30	97
gcc tta att cat gaa ggc att tta ttc aga tta acc ttc tgt aat tct Ala Leu Ile His Glu Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser 35 40 45	145
aac ata ata cat cac ttt tac tgt gac att atc cca ttg tta acg att Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Thr Ile 50 55 60	193
tcc tgt act gac cct tct att aat ttt tta atg ctt ttt att ttg tct Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser 65 70 75 80	241
ggt tca ata cag gta ttc act att ttg act gtt ctt gtc tct tat gca Gly Ser Ile Gln Val Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Ala 85 90 95	289
ttt gtc ctc ttt aca atc tta aaa aaa aag tca gtc aaa ggc ata agg Phe Val Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Lys Gly Ile Arg 100 105 110	337
aaa gcc ttt tcc acc tgt gga gcc cat ctc ttc tct gtc tgt tta tac Lys Ala Phe Ser Thr Cys Gly Ala His Leu Phe Ser Val Cys Leu Tyr 115 120 125	385
tat ggc ccc ctt ctc ttc atg tat gtg ggc cct gca tct cca caa gca Tyr Gly Pro Leu Leu Phe Met Tyr Val Gly Pro Ala Ser Pro Gln Ala 130 135 140	433
gat gat caa gat atg gta gag tgt gta ttt tac act gtc atc att cct Asp Asp Gln Asp Met Val Glu Cys Val Phe Tyr Thr Val Ile Ile Pro 145 150 155 160	481
ttc tta Phe Leu	487

<210> 156

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Leu Cys Ile Arg Leu Leu Val Leu Ser Phe Val Gly Gly Phe Leu His
Ala Leu Ile His Glu Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser
Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Thr Ile
Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser
                    70
Gly Ser Ile Gln Val Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Ala
Phe Val Leu Phe Thr Ile Leu Lys Lys Ser Val Lys Gly Ile Arg
                                 105
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Phe Ser Val Cys Leu Tyr
                            120
Tyr Gly Pro Leu Leu Phe Met Tyr Val Gly Pro Ala Ser Pro Gln Ala
    130
                        135
                                             140
Asp Asp Gln Asp Met Val Glu Cys Val Phe Tyr Thr Val Ile Ile Pro
Phe Leu
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<211> 487
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ctc tgc ctc ctg ctg gtc tcc ctc aca tac ctc tat ggc ttt tct aca
                                                                       97
Leu Cys Leu Leu Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr
get att gtg gtt tea eet tgt ata tte tet atg tet tat tge tet tet
                                                                      145
Ala Ile Val Val Ser Pro Cys Ile Phe Ser Met Ser Tyr Cys Ser Ser
aat ata atc aat cat ttt tac tgt gat att gca cct ctg tta gca tta
                                                                      193
Asn Ile Ile Asn His Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu
   50
                        55
tot tgo tot gat act tac tta oca gaa goa ata gto tto ata tot goa
                                                                      241
Ser Cys Ser Asp Thr Tyr Leu Pro Glu Ala Ile Val Phe Ile Ser Ala
gca aca aat ttg gtt ttt tcc atg att aca gtt cta gta tct tat ttc
                                                                      289
Ala Thr Asn Leu Val Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe
aat att gtt ttg tcc att cta agg atg cat tca tca gaa gga agg aaa
                                                                      337
Asn Ile Val Leu Ser Ile Leu Arg Met His Ser Ser Glu Gly Arg Lys
            100
                                105
aaa gcc ttt tcc acc tgt gct tca cat atg atg gca gtc aca gtt ttc
                                                                      385
Lys Ala Phe Ser Thr Cys Ala Ser His Met Met Ala Val Thr Val Phe
        115
                            120
tat ggg aca atg ctg ttc atg tat ttg cag ccc caa acc aac cac tca
Tyr Gly Thr Met Leu Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser
    130
ctg gat act gat aag atg gct tct gtg ttt tac aca ttg gtg att cct
                                                                      481
Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro
                    150
atg ctg
                                                                      487
Met Leu
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Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg
                5
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Leu Cys Leu Leu Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr

Ala	Ile	Val 35	Val	Ser	Pro	Cys	Ile 40	Phe	Ser	Met	Ser	Tyr 45	Сув	Ser	Ser		
Asn	Ile 50	Ile	Asn	His	Phe	Tyr 55	Cys	Asp	Ile	Ala	Pro 60	Leu	Leu	Ala	Leu		
Ser 65	Cys	Ser	Asp	Thr	Tyr 70	Leu	Pro	Glu	Ala	Ile 75	Val	Phe	Ile	Ser	Ala 80		
Ala	Thr	Asn	Leu	Val 85	Phe	Ser	Met	Ile	Thr 90	Val	Leu	Val	Ser	Tyr 95	Phe		
Asn	Ile	Val	Leu 100	Ser	Ile	Leu	Arg	Met 105	His	Ser	Ser	Glu	Gly 110	Arg	Lys		
Lys	Ala	Phe 115	Ser	Thr	Cys	Ala	Ser 120	His	Met	Met	Ala	Val 125	Thr	Val	Phe		
Tyr	Gly 130	Thr	Met	Leu	Phe	Met 135	Tyr	Leu	Gln	Pro	Gln 140	Thr	Asn	His	Ser		
Leu 145	Asp	Thr	Asp	Lys	Met 150	Ala	Ser	Val	Phe	Tyr 155	Thr	Leu	Val	Ile	Pro 160		
Met	Leu																
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	g go									ır Āl					cc atg co Met		49 ·
ctc Leu	tgt Cys	ctc Leu	gcc Ala	ctg Leu	gtg Val	gcg Ala	ctg Leu	tcc Ser	tgg Trp	gtg Val	ctg Leu	acc Thr	acc Thr	ttc Phe	cat His	:	97

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgc gca gac Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp

aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg  Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu  50  50  60	3
gcc tgc tct gac act cga gtc aat gaa ttg gtg ata ttt atc atg gga 24. Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly 65 70 75 80	1
ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca 289 Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 85 90 95	€
cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag ggt atc tgc 33 Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 100 105 110	7
aag gcg ttc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc 389 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125	5
tat ggg acc att att ggt ctc tac ttc tgc cca tca gct aat agt tct Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser 130 135 140	3
act cta aag gag act gtt atg ggt atg atg tac act gtg gtg acc ccc  Thr Leu Lys Glu Thr Val Met Gly Met Met Tyr Thr Val Val Thr Pro  145 150 155 160	L
atg ctg Met Leu	7
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	723
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<pre>&lt;223&gt; Taxon = 9557; gene = PPA140; Accession DDBJ/EMBL/GenBank = AF179 &lt;400&gt; 160 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met 1</pre>	723
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	Ile	Val	Ser 100	Ser	Ile	Leu	Lys	Val 105	Pro	Ser	Ser	Lys	Gly 110	Ile	Cys	
Lys	Ala	Phe 115	Ser	Thr	Cys	Gly	Ser 120	His	Leu	Ser	Val	Val 125	Ser	Leu	Phe	
Tyr	Gly 130	Thr	Ile	Ile	Gly	Leu 135	Tyr	Phe	Cys	Pro	Ser 140	Ala	Asn	Ser	Ser	
Thr 145	Leu	Lys	Glu	Thr	Val 150	Met	Gly	Met	Met	Tyr 155	Thr	Val	Val	Thr	Pro 160	
Met	Leu															
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<400 t gt	3> I 0> 1 cg ga	Produ 161 cc at	ıct = :c tç	olf t aa	ıg co	c tt	g aa	ac ta	at go yr Al	a Th	cc at nr Il	c at e Me	g ag et Se	gt ca er Gl	n Pro	49
<400 t gt Va 1 atg	3> I cg go al Al	Produ 161 cc at	ict = .c tg .e Cy	olf gt aa gt Ly 5 ctg	g co s Pr atg	c tto Le	g aa au As gtg	ac ta sn Ty gct	r Al 10 999	a Th	r Il	e Me	ttt	r Gl 15 gtg	n Pro cat	49 97
<400 t gt Va 1 atg Met	Cys  tgt  tgt	Produ 161 cc at la II	cc to ce Cy ttc Phe 20 cag	t aays Ly 5 ctg Leu	g co s Pr atg Met	ggg Gly ttc	g aa gtg Val ata	gct Ala 25	ggg Gly cag	att Ile tta	ctg Leu cca	gga Gly ttc	ttt Phe 30	er Gl 15 gtg Val	n Pro cat His	
<400 t gt Va 1 atg Met gga Gly	3> I cg gc al Al tgt Cys ggg Gly	Production of the second secon	ttc Phe 20 cag Gln	t aars Ly 5 ctg Leu act Thr	ag co s Pr atg Met ctg Leu	ggg Gly ttc Phe	gtg Val ata Ile 40	gct Ala 25 gcc Ala	ggg Gly cag Gln tta	att Ile tta Leu	ctg Leu cca Pro	gga Gly ttc Phe 45	ttt Phe 30 tgt Cys	gtg Val ggc Gly	cat His ccc Pro	97
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atc atc ctg tgc tcc cta agg act cat atc tct gaa ggg cgt cac aaa Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys

gct ctg tct agt tgt acc tct cat atc ttt gtt gtc atc tta ttc ttt Ala Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe 115 120 125	
gtc cct tgt tca tac ctg tat cta aga cct cta acc tcc ttc ccc act Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Pro Thr 130 135 140	
gac aaa gct gtg act gtg ttt tgc acc cta ttt aca cct atg ttg Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu 145 150 155	
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Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro 35 40 45	
Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu 50 55 60	
Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser 65 70 75 80	
Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val 85 90 95	
Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys 100 105 110	
Ala Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe 115 120 125	
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                                       10
gtc tgc aca ctg ctt gtt ttt act tct tgg ctg gtt tca ttc tta atc
                                                                       97
Val Cys Thr Leu Leu Val Phe Thr Ser Trp Leu Val Ser Phe Leu Ile
            20
                                 25
ata ttc cca gca ctc atg ttg ctc tta cag ctt gat tac tgt agg tct
                                                                      145
Ile Phe Pro Ala Leu Met Leu Leu Gln Leu Asp Tyr Cys Arg Ser
aat att atg gac cat ttt acc tgt gat tat ttt ccc ctg ctg caa ctt
                                                                      193
Asn Ile Met Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
                        55
gct tgt tca gac aca aaa ttc cta gag gtg atg gga ttt tct tgt gct
                                                                      241
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Gly Phe Ser Cys Ala
gtg ttt act cta atg ttg act ttg gca tta ata ttt ctg tcc tac ata
                                                                      289
Val Phe Thr Leu Met Leu Thr Leu Ala Leu Ile Phe Leu Ser Tyr Ile
                85
tac att atc aga aca att ttg aga att cct tct gct agt caa agg aca
                                                                      337
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Thr
                                105
aag goo ttt too aca tgt tot too cac atg att gto ato too atc tot
                                                                      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
                            120
tat ggc agc tgc att ttt atg tac att aaa ccc tca gca aaa gat aga
                                                                      433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
                        135
gtg tcc ttg agc aag gga gtg gca ata cta aac acc tca gta gcc ccc
                                                                      481
Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Āla Pro
145
                    150
                                        155
atg ctg
                                                                      487
Met Leu
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Val Cys Thr Leu Leu Val Phe Thr Ser Trp Leu Val Ser Phe Leu Ile
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Ile Phe Pro Ala Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Arg Ser
Asn Ile Met Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Gly Phe Ser Cys Ala
                    70
Val Phe Thr Leu Met Leu Thr Leu Ala Leu Ile Phe Leu Ser Tyr Ile
                85
                                    90
                                                        95
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Thr
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
Met Leu
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                                                                      49
 Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp
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1				5					10	)				15	5		
	tgc Cys															!	97
_	acc Thr			_										_	_	1	45
	atc Ile 50															19	93
	agt Ser															24	41
_	gtc Val			_					_		_					21	39
_	atc Ile	-		-				_	-			_	_	_	_	3:	37
_	gtc Val				_				_			_				38	35
	gga Gly 130															43	33
_	acc Thr		_	_	_		_					_				48	31
atg Met																4 8	37
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Ala	Cys	Met	Ala 20	Met	Val	Gly	Thr	Ser 25	Trp	Leu	Thr	Gly	Ile 30	Ile	Thr		
Ala	Thr	Thr 35	His	Ala	Phe	Leu	Ile 40	Phe	Ser	Leu	Pro	Phe 45	Pro	Ser	Arg		

Pro	Ile 50	Ile	Pro	His	Phe	Leu 55	Cys	Asp	Ile	Leu	Pro 60	Val	Leu	Arg	Leu	
Ala 65	Ser	Ala	Gly	Lys	His 70	Arg	Ser	Glu	Ile	Ser 75	Val	Met	Thr	Ala	Thr 80	
Val	Val	Phe	Ile	Met 85	Ile	Pro	Phe	Ser	Leu 90	Ile	Val	Thr	Ser	Tyr 95	Ile	
Arg	Ile	Leu	Gly 100	Ala	Ile	Leu	Ala	Met 105	Ala	Ser	Thr	Gln	Ser 110	Arg	Arg	
Lys	Val	Phe 115	Ser	Thr	Cys	Ser	Ser 120	His	Leu	Leu	Val	Val 125	Ser	Leu	Phe	
Phe	Gly 130	Thr	Ala	Ser	Ile	Thr 135	Tyr	Ile	Arg	Pro	Gln 140	Ala	Gly	Ser	Ser	
Val 145	Thr	Thr	Asp	Arg	Val 150	Leu	Ser	Leu	Phe	Tyr 155	Thr	Val	Ile	Thr	Pro 160	
Met	Leu															
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<220 <220 <220 <220	L> ( 2> (		.(487 ict =	_	facto	ory r	ecer	otor								
	g go									ır Al					cc atg	49
					gtg Val											97
					tta Leu											145
					ttt Phe											193
					cga Arg 70											241

ggg ctc att gtt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 85 90 95	289
aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 100 105 110	337
aag gcc ttg tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125	385
tat ggg acc gtt att ggt ctc tac tta tgc cca tca gct aat agt tct Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser 130 135 140	433
act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 145 150 155 160	481
atg ctg Met Leu	487
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-	F1/9/2/
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Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met	F1/9/2/
Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met  1 5 10 15  Leu Cys Leu Ser Val Val Thr Leu Ser Trp Val Leu Thr Thr Phe His	F1/9/2/
Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met 1 5 10 10 15  Leu Cys Leu Ser Val Val Thr Leu Ser Trp Val Leu Thr Thr Phe His 20  Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp	F1/9/2/
Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met 15  Leu Cys Leu Ser Val Val Thr Leu Ser Trp Val Leu Thr Thr Phe His 20  Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 40  Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Leu Leu	F1/9/2/
Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met 15  Leu Cys Leu Ser Val Val Thr Leu Ser Trp Val Leu Thr Thr Phe His 30  Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 45  Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 50  Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly	F1/9/2/
Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met 15  Leu Cys Leu Ser Val Val Thr Leu Ser Trp Val Leu Thr Thr Phe His 30  Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 40  Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 55  Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly 80  Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala	F1/9/2/

115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser 130 135 140

Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

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ctc tgt ctc tcc gtg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
                                                                          97
Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                                 25
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac
                                                                         145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
                             40
aat gtg atc ccc cac ttt ttc tgt gat atg tct gct cta ctg aag ctg
                                                                         193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
    50
gcc tgc tct gac act cga gtt aat gaa tgg gtg ata ttt atc atg gga Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
                                                                         241
ggg ctc att gtt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca
                                                                         289
Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                                      90
aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc
                                                                         337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
            100
                                 105
aag gcc ttg tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc
                                                                         385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
tat ggg acc gtt att ggt ctc tac tta tgc cca tca gct aat agt tct
                                                                         433
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser
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atg ctg Met Leu				487
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Ala Met Leu His Thr 35	Leu Leu Met A 40		Phe Cys Ala Asp	
Asn Val Ile Pro His 50	Phe Phe Cys A 55	asp Met Ser Ala L 60	eu Leu Lys Leu	
Ala Cys Ser Asp Thr 65	Arg Val Asn G 70	lu Trp Val Ile P 75	Phe Ile Met Gly 80	
Gly Leu Ile Val Val 85	Ile Pro Phe L	eu Leu Ile Leu G 90	Gly Ser Tyr Ala 95	
Arg Ile Val Ser Ser 100	<del>-</del>	al Pro Ser Ser L 05	ys Gly Ile Cys 110	
Lys Ala Leu Ser Thr 115	Cys Gly Ser H		al Ser Leu Phe .25	
Tyr Gly Thr Val Ile 130	135	140		·
Thr Leu Lys Asp Thr 145	Val Met Ala Mo 150	let Met Tyr Thr V 155	al Val Thr Pro 160	

Met Leu

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                                                                      120
attgcgacta actitictgca ggtttaacat aatacattat ttctactgtg aaattttaca
                                                                      180
actgttcaaa atttcatgca atggtccatc tattaacgca ctaatgatat ttatttttgg
                                                                      240
tgcttttata caaataccca ctttaatgac gatcataatc tcttatactc gtgtgctctt
                                                                      300
tgatattetg aaaaaaaagt etgaaaaggg cagaagcaaa geetteteca catgeagege
                                                                      360
ccatctgctt tctgtctcat tgtactacgg aactctgatc ttcatqtatq tqcqtcctgc
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tgcta
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gto tgt goo ota atg ott goa ttg tgo tgg gto oto acc aat ato att
                                                                       97
Val Cys Ala Leu Met Leu Ala Leu Cys Trp Val Leu Thr Asn Ile Ile
gee etg act cae acg tte etc atg get egg ttg tee tte tgt gtg act
                                                                      145
Ala Leu Thr His Thr Phe Leu Met Ala Arg Leu Ser Phe Cys Val Thr
        35
                            40
ggg gaa att gct cac ttt ttc tgt gac atc act cct gtc ctg aag ctg
                                                                      193
Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
                        55
tca tgt tct gac acc cac atc aac gag atg atg gtt ttt gtc ttg gga
                                                                      241
Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
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75

Gly Thr Val Leu Ile Val Pro Ph 85	t tta tgc att gt ne Leu Cys Ile Va 90	c acc tcc tac atc 289 l Thr Ser Tyr Ile 95
cac att gtg cca gct atc ctg ag His Ile Val Pro Ala Ile Leu Ar 100		
aag gcc ttt tcc acc tgc agt tc Lys Ala Phe Ser Thr Cys Ser Se 115	er His Leu Cys Va	
tat ggg acg ctc ttc agt gcc ta Tyr Gly Thr Leu Phe Ser Ala Ty 130		o Ser Ile Ala Ser
gaa gag aag gac att gca gca gc Glu Glu Lys Asp Ile Ala Ala Al 145 150		
atg ttg Met Leu		487
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<pre>&lt;222&gt; (1)(487) &lt;223&gt; Taxon = 9598; gene = PT &lt;400&gt; 173 Val Ala Ile Cys Arg Pro Leu Cy 1</pre>	s Tyr Ser Thr Val 10 u Cys Trp Val Leu 25 t Ala Arg Leu Ser	Thr Arg Pro Gln 15  Thr Asn Ile Ile 30  Phe Cys Val Thr 45
<pre>&lt;222&gt; (1)(487) &lt;223&gt; Taxon = 9598; gene = PT &lt;400&gt; 173 Val Ala Ile Cys Arg Pro Leu Cy 1</pre>	s Tyr Ser Thr Val 10  u Cys Trp Val Leu 25  t Ala Arg Leu Ser s Asp Ile Thr Pro	Thr Arg Pro Gln 15  Thr Asn Ile Ile 30  Phe Cys Val Thr 45  Val Leu Lys Leu
<pre>&lt;222&gt; (1)(487) &lt;223&gt; Taxon = 9598; gene = PT &lt;400&gt; 173 Val Ala Ile Cys Arg Pro Leu Cy 1</pre>	s Tyr Ser Thr Val 10  u Cys Trp Val Leu 25  t Ala Arg Leu Ser s Asp Ile Thr Pro 60  n Glu Met Met Val 75	Thr Arg Pro Gln 15  Thr Asn Ile Ile 30  Phe Cys Val Thr 45  Val Leu Lys Leu Phe Val Leu Gly 80

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Cys Val Phe 115 120 125

Tyr	Gly	Thr	Leu	Phe	Ser	Ala	Tyr	Leu	Cys	Pro	Pro	Ser	Ile	Ala	Ser
	130					135					140				

Glu Glu Lys Asp Ile Ala Ala Ala Ala Met Tyr Thr Ile Val Thr Pro
145 150 155 160

Met Leu

<210><211><211><212><213>	174 487 DNA Pan tr	oglody	'tes												
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ctc tgt Leu Cys	gcc to Ala Se 20	er Leu	gta Val	gct Ala	gca Ala	cct Pro 25	tgg Trp	gtc Val	att Ile	gcc Ala	att Ile 30	ttg Leu	aac Asn	97	
cct ctc Pro Lei	ttg ca Leu H: 35	ac act is Thr	ctt Leu	atg Met	atg Met 40	gcc Ala	cat His	ctg Leu	cac His	ttc Phe 45	tgc Cys	tct Ser	gat Asp	145	
aat gtt Asn Val 50	atc ca Ile Hi	ac cat is His	ttc Phe	ttc Phe 55	tgt Cys	gat Asp	atc Ile	aac Asn	tct Ser 60	ctc Leu	ctc Leu	cct Pro	ctg Leu	193	
tcc tgt Ser Cys 65	tcc aa Ser As	ac acc sn Thr	agt Ser 70	ctt Leu	aat Asn	cag Gln	ttg Leu	agt Ser 75	gtt Val	ctg Leu	gct Ala	acg Thr	gtg Val 80	241	
ggg ctg Gly Leu	atc tt	t gtg ne Val 85	gta Val	cct Pro	tca Ser	gtg Val	tgt Cys 90	atc Ile	ctg Leu	gta Val	tcc Ser	tat Tyr 95	atc Ile	289	
ctc att Leu Ile	gtt to Val Se	er Ala	gtg Val	atg Met	aaa Lys	gtc Val 105	cct Pro	tct Ser	gcc Ala	caa Gln	gga Gly 110	aaa Lys	ctc Leu	337	
aag gct Lys Ala	ttc to Phe Se 115	ct atc er Ile	tgt Cys	gga Gly	tct Ser 120	cac His	ctt Leu	gcc Ala	ttg Leu	gtc Val 125	att Ile	ctt Leu	ttc Phe	385	
tat gga Tyr Gly 130	gca at Ala Il	c aca e Thr	gly aaa	gtc Val 135	tat Tyr	atg Met	agc Ser	ccc Pro	tta Leu 140	tcc Ser	aat Asn	cac His	tct Ser	433	

<210> 176 <211> 487

act Thi	GII	a aaa ı Lys	a gad s Asp	c tca p Ser	Ala 150	ı Ala	tca Ser	gto Val	att l Ile	ttt Phe	e Met	g gtt : Va]	gta Val	gca Ala	cct Pro 160	481
	g ttg . Lei															487
<21 <21 <21 <21	1> 2>	175 162 PRT Pan	trog	Jlody	tes											
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<40 Val 1		175 Ile	Cys	His 5	Pro	Leu	His	Tyr	Ser 10	Thr	Ile	Met	Ala	Leu 15	Arg	
Leu	Суѕ	Ala	Ser 20	Leu	Val	Ala	Ala	Pro 25	Trp	Val	Ile	Ala	Ile 30	Leu	Asn	
Pro	Leu	Leu 35	His	Thr	Leu	Met	Met 40	Ala	His	Leu	His	Phe 45	Cys	Ser	Asp	
Asn	Val 50	Ile	His	His	Phe	Phe 55	Сув	Asp	Ile	Asn	Ser 60	Leu	Leu	Pro	Leu	
Ser 65	Cys	Ser	Asn	Thr	Ser 70	Leu	Asn	Gln	Leu	Ser 75	Val	Leu	Ala	Thr	Val 80	
Gly	Leu	Ile	Phe	Val 85	Val	Pro	Ser	Val	Cys 90	Ile	Leu	Val	Ser	Tyr 95	Ile	
Leu	Ile	Val	Ser 100	Ala	Val	Met	Lys	Val 105	Pro	Ser	Ala	Gln	Gly 110	Lys	Leu	
Lys	Ala	Phe 115	Ser	Ile	Сув	Gly	Ser 120	His	Leu	Ala	Leu	Val 125	Ile	Leu	Phe	
Tyr	Gly 130	Ala	Ile	Thr	Gly	Val 135	Tyr	Met	Ser	Pro	Leu 140	Ser	Asn	His	Ser	
Thr 145	Glu	Lys	Asp	Ser	Ala 150	Ala	Ser	Val	Ile	Phe 155	Met	Val	Val	Ala	Pro 160	
Val	Leu															

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<221>
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       (1)..(487)
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       (2)..(487)
<222>
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t gtg gcg gtg tgt aac cct ctt ctc tac aca gtt gca atg tac cag agg
                                                                             49
  Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg
ctt tgc tcc ttg ttg gtg gct aca tca tac tgt tgg ggg aga gtc tgt
                                                                             97
Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Cys Trp Gly Arg Val Cys
tcc ctg aca ctt acc tac ttt cta ctg gaa tta tcc ttc aga gga aat
                                                                            145
Ser Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
                                                                            193
aat atc att aat aac ttt gtc tgt gag cat gct gcc att gtt gct gtg
Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
                                                60
tct tgc tct gac ccc tat gtg agc cag gag atc act tta gtt tct gcc Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
                                                                            241
aca ttc aat gaa ata agc agc ctg gtg atc act ctc act tcc tat gct Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Thr Leu Thr Ser Tyr Ala
                                                                            289
                 85
                                                                            337
ttc att ttt atc act gtc atg aag acg gct tcc att ggg ggg cgc aag
Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Ile Gly Gly Arg Lys
             100
                                   105
aaa geg tte tte acg tgt gee tee cae ttg acg gee att ace att tte
                                                                            385
Lys Ala Phe Phe Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
                               120
                                                                            433
cat ggg act att ctt ttc ctc tac tgt gtt cct aac tcc aaa agt tcg
His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Ser Ser
                          135
                                                140
tgg ctc atg gtc aag gtg gcc tct gtc ttt tac aca gtg gtc att ccc
                                                                            481
Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro
                                                                            487
atg ctg
Met Leu
<210> 177
<211> 162
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<221> misc\_feature



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<222> (1)..(487)
<223> Taxon = 9598; gene = PTR207; Accession DDBJ/EMBL/GenBank = AF179732
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Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Cys Trp Gly Arg Val Cys 20 25 30

Ser Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn 35 40 45

Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val 50 55 60

Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala 65 70 75 80

Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Thr Leu Thr Ser Tyr Ala 85 90 95

Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Ile Gly Gly Arg Lys
100 105 110

Lys Ala Phe Phe Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe 115 120 125

His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Ser Ser 130 135 140

Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro 145 150 155 160

Met Leu

- <210> 178
- <211> 481
- <212> DNA
- <213> Pan troglodytes
- <220>
- <221> misc\_feature
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- <223> Taxon = 9598; gene = PTR208; Accession DDBJ/EMBL/GenBank = AF179733
- <220>
- <221> CDS
- <222> (2)..(481)
- <223> Product = olfactory receptor
- <400> 178
- c ctg gca ata tgt cag ccc ctg cgc tac cca gtg ctc atg aat ggg agg Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg

					gtg Val							97
					acc Thr							145
					ttt Phe							193
					act Thr 70							241
					agt Ser							289
					atc Ile							337
					tgt Cys							385
	_		_		ttc Phe			_				433
					gct Ala 150							481
<210 <211 <212 <213	> 1 2> E	179 160 PRT Pan t	rogl	Lodyt	es							
<220	)>											

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Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg

Leu Cys Thr Val Leu Val Ala Gly Ala Cys Val Ala Gly Ser Met His

Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro

Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu

Ala 65	. Cys	a Ala	Asp	Thr	Thr 70	Val	Asn	Glu	. Leu	Val 75	Thr	Phe	· Val	. Asp	Val 80		
Gly	Val	. Val	Ala	Ala 85	Ser	Cys	Phe	Met	Leu 90	Ile	Leu	ı Leu	Ser	Tyr 95	Ala		
Asn	Ile	· Val	Asn 100	Ala	Ile	Leu	Lys	Ile 105		Thr	Thr	Asp	Gly 110	Arg	His		
Arg	Ala	Phe 115		Thr	Cys	Gly	Ser 120		Leu	Ile	Val	Val 125		Val	Tyr		
Tyr	Val 130		Сув	Ile	Phe	Ile 135		Leu	Arg	Ala	Gly 140		Lys	Gly	Pro		
Leu 145	Asp	Gly	Ala	Ala	Ala 150	Val	Phe	Tyr	Thr	Val 155	Val	Thr	Pro	Leu	Leu 160		
<21 <21 <21 <21	1 > 2 >	180 487 DNA Pan	trog:	lody	ces						-						
<22 <22 <22 <22	1> 1 2>	(1).	_feat .(48' n = 5	7)	; gei	ne =	PTR	209;	Acc	essi	on D	DBJ/	EMBL	/GenI	3ank =	• AF179	<del>)</del> 734
<22 <22 <22 <22	1 > ( 2 >	_	.(487 uct =		acto	ory i	cecep	ptor									
<40 c g v 1	tg go	180 cc at la I	tc to	gt ca ys Hi 5	ac co .s Pi	ec ct	g ta eu Ty	ac ta yr Ty	ac co yr Ai 10	rg Va	cc at al I	tc gi le Va	ng aa	ac co sn Pr 15	cc cgc co Arg	4	19
ctc Leu	tgt Cys	ggc Gly	ctg Leu 20	ctg Leu	gtt Val	ctt Leu	gtg Val	tcc Ser 25	tgg Trp	ttc Phe	ctc Leu	agc Ser	ttg Leu 30	tca Ser	tac Tyr	9	7
tcc Ser	ctg Leu	atc Ile 35	cag Gln	agt Ser	ctg Leu	ttg Leu	atg Met 40	ctg Leu	cag Gln	gtg Val	tcc Ser	ttc Phe 45	tgt Cys	acc Thr	agt Ser	14	:5
tgg Trp	gtc Val 50	att Ile	cag Gln	cac His	ttt Phe	tac Tyr 55	tgt Cys	gag Glu	ctt Leu	gct Ala	cag Gln 60	gtc Val	ctc Leu	acg Thr	ctt Leu	19	3
acc Thr 65	tgc Cys	tca Ser	gac Asp	aca Thr	cac His 70	gtc Val	aat Asn	tac Tyr	atc Ile	ctg Leu 75	ctg Leu	tac Tyr	gtg Val	gtg Val	act Thr 80	24	1
ggc Gly	ctt Leu	ctg Leu	gac Asp	ttt Phe 85	gtg Val	ccc Pro	ttc Phe	tca Ser	90 999 999	atc Ile	ctt Leu	ttc Phe	tcc Ser	tac Tyr 95	acc Thr	28	9
caa Gln	att Ile	gtc Val	tcc Ser	tac Tyr	atc Ile	cta Leu	aga Arg	atc Ile	tca Ser	tcc Ser	aca Thr	gat Asp	999 Gly	aaa Lys	cac His	33	7

							gtt Val 125			385
					_		gca Ala	_		433
							gtg Val			481
atg	ctg									487

Met Leu

<210> 181 <211> 162 <212> PRT

<213> Pan troglodytes

<220>

<221> misc\_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR209; Accession DDBJ/EMBL/GenBank = AF179734

<400> 181

Val Ala Ile Cys His Pro Leu Tyr Tyr Arg Val Ile Val Asn Pro Arg

Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr

Ser Leu Ile Gln Ser Leu Leu Met Leu Gln Val Ser Phe Cys Thr Ser 40

Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu 50 55

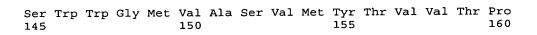
Thr Cys Ser Asp Thr His Val Asn Tyr Ile Leu Leu Tyr Val Val Thr

Gly Leu Leu Asp Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr

Gln Ile Val Ser Tyr Ile Leu Arg Ile Ser Ser Thr Asp Gly Lys His

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Phe Val Val Ser Leu Phe

Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser 130



Met Leu

<210> 182 <211> 487 <212> DNA <213> Pan troglodytes	
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<220> <221> CDS <222> (2)(487) <223> Product = olfactory receptor	
<pre>&lt;400&gt; 182 t gta gcc ata tgt aat ccc ttg ctt tat cca gtg atg atg tcc aac aaa   Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys   1 5 10 15</pre>	49
ctc agc gct cag ttg cta agc att tca tat gta att ggt ttc ctg cat Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His 20 25 30	97
cct ctg gtt cat gtg agt tta cta ttg cga cta act ttc tgc agg ttt Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe 35 40 45	145
aac ata ata cat tat ttc tac tgt gaa att tta caa ctg ttc aaa att Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile 50 55 60	193
tca tgc aat ggt cca tct att aac gca cta atg ata ttt att ttt ggt Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly 65 70 75 80	241
gct ttt ata caa ata ccc act tta atg acg atc ata atc tct tat tct Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser 85 90 95	289
cgt gtg ctc ttt gat att ctg aaa aaa aag tct gaa aag ggc aga agc Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser 100 105 110	337
aaa gcc ttc tcc aca tgc agc gcc cat ctg ctt tct gtc tca ttg tac Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr 115 120 125	385
tac gga act ctg atc ttc atg tat gtg cgt cct gca tct ggc tta gct Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala 130 135 140	433
gaa gac cca gac aaa gtg tat tct ctg ttt tac acg att ata att ccc Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro 145 150 155 160	481
ctg cta Leu Leu	487

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Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly
Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser
                                     90
Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
                                 105
Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr
        115
                            120
Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
                        135
Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
                    150
Leu Leu
<210> 184
<211>
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<213> Pan troglodytes
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       Product = olfactory receptor
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  Val Ala Ile Cys His Pro Leu Arg Tyr Thr Val Leu Met Asn Ile His
                                        10
tte tge gge ttg etg att ett ete tee agg tte atg age act atg gat
                                                                          97
Phe Cys Gly Leu Leu Ile Leu Leu Ser Arg Phe Met Ser Thr Met Asp
                                 25
gcc ctg gtt cag agt ctg atg ata ttt cag ctg tcc ttc tgc aaa aac
                                                                         145
Ala Leu Val Gln Ser Leu Met Ile Phe Gln Leu Ser Phe Cys Lys Asn
gtt gaa atc cct ttg ttc ttc tgt gaa gtc gtt cag gtc atc aag ctc Val Glu Ile Pro Leu Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu
                                                                         193
                         55
gcc tgt tct gac acc ctc atc aac aac atc ctc ata tat ttt gca agt
                                                                         241
Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser
                     70
age ata ttt ggt gea att eet ete tet gga ata att tte tet tat tet
                                                                         289
Ser Ile Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser
                85
                                      90
caa ata gtc acc tct gtt ctg aga atg cca tca gca aga gga aag tat
                                                                         337
Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr
            100
                                                                         385
aaa geg ttt tee ace tgt gge tgt cae ete tet gtt ttt tee ttg tte
Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe
        115
tat ggg aca gct ttt ggg gtg tcc att agt tct gct gtt gct gag tct
                                                                         433
Tyr Gly Thr Ala Phe Gly Val Ser Ile Ser Ser Ala Val Ala Glu Ser
tcc cga att act gct gtg ggt tca gtg atg tac act gtg gtc cca caa
                                                                         481
Ser Arg Ile Thr Ala Val Gly Ser Val Met Tyr Thr Val Val Pro Gln
                     150
                                          155
                                                                         487
atg atg
Met Met
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<211> 162
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Val Ala Ile Cys His Pro Leu Arg Tyr Thr Val Leu Met Asn Ile His
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Phe Cys Gly Leu Leu Ile Leu Leu Ser Arg Phe Met Ser Thr Met Asp
Ala Leu Val Gln Ser Leu Met Ile Phe Gln Leu Ser Phe Cys Lys Asn
        35
                            40
Val Glu Ile Pro Leu Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu
Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser
Ser Ile Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser
Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr
                                105
Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe
        115
                            120
Tyr Gly Thr Ala Phe Gly Val Ser Ile Ser Ser Ala Val Ala Glu Ser
Ser Arg Ile Thr Ala Val Gly Ser Val Met Tyr Thr Val Val Pro Gln
                    150
                                        155
Met Met
<210> 186
<211> 487
<212> DNA
<213> Pan troglodytes
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<223> Product = olfactory receptor
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t gtt gcc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag
                                                                       49
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97

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu

ctc tgt gtc ttc tta gtg gct gta tct tgg att ctg tct tgt gcc agc

Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser

tcc Ser	ctc Leu	tct Ser 35	cac His	acc Thr	ctt Leu	ctc Leu	ctg Leu 40	acc Thr	cgg Arg	ctg Leu	tct Ser	ttc Phe 45	tgt Cys	gct Ala	gcg Ala		145
aac Asn	acc Thr 50	atc Ile	ccc Pro	cat His	gtc Val	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	gct Ala	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu		193
tcc Ser 65	tgc Cys	tca Ser	gat Asp	atc Ile	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttc Phe	aca Thr	gta Val	80 Gly 333		241
gtg Val	gtg Val	gtc Val	att Ile	acc Thr 85	ctg Leu	cca Pro	ttc Phe	atg Met	tgt Cys 90	atc Ile	ctg Leu	gta Val	tca Ser	tat Tyr 95	ggc Gly		289
tac Tyr	att Ile	Gly 999	gcc Ala 100	acc Thr	atc Ile	ctg Leu	agg Arg	gtc Val 105	cct Pro	tca Ser	acc Thr	aaa Lys	999 Gly 110	atc Ile	cac His		337
												gtg Val 125					385
tat Tyr	999 Gly 130	tca Ser	ata Ile	ttt Phe	ggc Gly	cag Gln 135	tac Tyr	ctt Leu	ttc Phe	ccg Pro	act Thr 140	gta Val	agc Ser	agt Ser	tct Ser		433
att Ile 145	gac Asp	aag Lys	gat Asp	gtc Val	att Ile 150	gtg Val	gct Ala	ctc Leu	atg Met	tac Tyr 155	acg Thr	gtg Val	gtc Val	aca Thr	ccc Pro 160		481
atg Met	_				٠												487
<210 <211 <212 <213	> 1 > F	.87 .62 PRT Pan t	rogl	odyt	es												
<220 <221 <222 <223	> m	1)	feat (487 (= 9	)	gen	.e =	PTR2	12;	Acce	ssic	on DI	)BJ/E	MBL/	GenE	ank	= AF	179737
<400 Val 1	> 1	87										Met					
Leu	Cys	Val	Phe 20	Leu	Val	Ala	Val	Ser 25	Trp	Ile	Leu	Ser	Cys 30	Ala	Ser		
Ser	Leu	Ser 35	His	Thr	Leu		Leu 40	Thr	Arg	Leu	Ser	Phe 45	Cys	Ala	Ala		
Asn	Thr 50	Ile	Pro	His		Phe 55	Cys	Asp	Leu		Ala 60	Leu	Leu	Lys	Leu		
Ser 65	Cys	Ser	Asp		Phe 70	Leu	Asn	Glu		Val 75	Met	Phe	Thr	Val	Gly 80		

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Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                                    90
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
            100
                                105
                                                    110
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
        115
                            120
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
                                        155
Met Leu
<210>
      188
<211>
      484
<212>
      DNA
<213> Hylobates lar
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= AF179738
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                                                                      60
gatggcagca ctgagctggg ggacaggctt tgccaactca ctgctacagt ccatccttgt
                                                                      120
ctggcgcctc cctttctgtg gccacaacgt catcaaccac tttttctgtg agatcttggc
                                                                      180
agtgctaaaa ctggcctgtg gggacatctc cctcaatgcg ctggcattaa tggtggccac
                                                                      240
agetyteety acaetygeee ecetettyet catetycety tettacettt teatettyte
                                                                     300
tgccatcctt agggtaccct ctgctgcagg ccggcgcaaa gccttctcca cctgctcagc
                                                                     360
ccacctcaca gtggtggtgg ttttttaagg gacaatttcc ttcatgtact tcaaacccaa
                                                                      420
ggccaaggac cccaacgtgg ataagattgt tgcattgttg tatggggttg tgacaccctc
                                                                      480
gctg
                                                                      484
<210>
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<211>
      487
<212>
      DNA
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<210> 189
<211> 487
<212> DNA
<213> Hylobates lar
<220>
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<222> (1)..(487)
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<223> Taxon = 9580; gene = HLA122; Accession DDBJ/EMBL/GenBank = AF179739

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<222> (2)
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 <223> Product = olfactory receptor
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   Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg
                                         10
 ctt tgc tcc ttg ttg gtg gct aca tca tac tct tgg ggg ata gtc tgt
                                                                           97
 Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys
             20
                                   25
 ttc ctg aca ctt acc tac ttt cta ctg gaa tta tcc ttc aga gga aat
                                                                          145
 Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
 aat atc att aat aac ttt gtc tgt gag cat gct gcc att gtt gct gtg
                                                                          193
 Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
     50
 tet tge tet gae eee tat gtg age eag gag ate act tta gtt tet gee
                                                                          241
 Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
aca ttc aat gaa ata agc agt ctg atg atg att ttc act tcc tat gct
                                                                          289
Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala
                                      90
ttc att ttt atc act gtc atg aag atg cct tcc act ggg ggg cgc aag
                                                                         337
Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys
                                  105
aaa gcg ttc tcc acg tgt gcc tcc cac ctg acc gcc att acc att ttc
                                                                         385
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
        115
cat ggg act atc ctt ttc ccc tac tgt gtt cct aac tcc aaa agt tca
His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser
tgg ctc atg gtc aag gtg acc tct gtc ttt tac aca gtg ttc att ccc Trp Leu Met Val Lys Val Thr Ser Val Phe Tyr Thr Val Phe Ile Pro
                                                                         481
                                          155
atg gtg
                                                                         487
Met Val
<210> 190
<211> 162
<212> PRT
<213> Hylobates lar
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       Taxon = 9580; gene = HLA122; Accession DDBJ/EMBL/GenBank = AF179739
<400> 190
Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg
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Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys
                                 25
 Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
 Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
 Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala
                                     90
Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys
            100
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
        115
His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser
                        135
Trp Leu Met Val Lys Val Thr Ser Val Phe Tyr Thr Val Phe Ile Pro
Met Val
<210> 191
<211> 486
<212> DNA
<213> Hylobates lar
<220>
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      (2)..(484)
<223> Product = olfactory receptor
<400> 191
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                                                                       49
 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
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145

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp

		35					40					45					
	atc Ile 50																193
	tgc Cys							_	_	_				_			241
	aca Thr																289
	att Ile																337
	gcc Ala																385
	ggg Gly 130																433
	gac Asp																481
atg Met	tt																486
<210 <211 <212 <213	l> 1 2> F	.92 .61 PRT Iylob	oates	s lar	<del>.</del>												
<220 <221 <222 <223	-> π 2> (	1)	_feat (486 1 = 9	5)	ger	ie =	HLA1	.23;	Acce	essic	on DI	BJ/E	EMBL/	'GenE	Bank	= AF	179740
<400 Val 1	)> 1 Ala	.92 Ile	Cys	His 5	Pro	Leu	His	Tyr	Ala 10	Thr	Ile	Met	Ser	Gln 15	Ser		
Gln	Cys	Val	Met 20	Leu	Val	Ala	Gly	Ser 25	Trp	Val	Ile	Ala	Cys 30	Ala	Cys		
Ala	Leu	Leu 35	His	Thr	Leu	Leu	Leu 40	Ala	Gln	Leu	Ser	Phe 45	Cys	Ala	Asp		
His	Ile 50	Ile	Pro	His	Phe	Phe 55	Cys	Asp	Leu	Gly	Ala 60	Leu	Leu	Lys	Leu		

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 70 80

85	u Pro Phe Leu Cy 90	ys Ile Leu Val Ser O	Tyr Gly 95
His Ile Gly Val Thr Il 100	e Leu Gln Ile Pi 105	ro Ser Thr Lys Gly	Ile Cys
Lys Ala Leu Ser Thr Cy 115	s Gly Ser His Le 120	eu Ser Val Val Thr 125	Ile Tyr
Tyr Gly Thr Ile Ile Gl 130	y Leu Tyr Phe Le 135	eu Pro Pro Ser Ser . 140	Asn Thr
Asn Asp Lys Asn Ile Il 145 15		le Tyr Thr Val Val 155	Thr Pro 160
Met			
<210> 193 <211> 487 <212> DNA <213> Hylobates lar			
<220> <221> misc_feature <222> (1)(487)	W.N.104 No.		
<223> Taxon = 9580; g	ene = HLAI24; AC	ccession DDBJ/EMBL/	GenBank = AF179741
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<220> <221> CDS <222> (2)(487)	tory receptor	cca gtc atc atg aa	c caa agg 49
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<220> <221> CDS <222> (2)(487) <223> Product = olface <400> 193 t gtg gcc atc tgt agt    Val Ala Ile Cys Ser    1	tory receptor  ccc ttg cac tac  Pro Leu His Tyr  t gct gcc tcc tc a Ala Ala Ser Tr 25 a tgg ctc ttc ac	cca gtc atc atg aad Pro Val Ile Met Ass 10 gg ttc cca ggc ttt o rp Phe Pro Gly Phe 1 30 gt ttt cca ttc tgt o	c caa agg 49 n Gln Arg 15 cct gta 97 Pro Val
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<pre>&lt;220&gt; &lt;221&gt; CDS &lt;222&gt; (2)(487) &lt;223&gt; Product = olface &lt;400&gt; 193 t gtg gcc atc tgt agt    Val Ala Ile Cys Ser    1</pre>	tory receptor  ccc ttg cac tac Pro Leu His Tyr  t gct gcc tcc tg a Ala Ala Ser Tr 25 a tgg ctc ttc ag r Trp Leu Phe Se 40 c ttc tgt gac ag e Phe Cys Asp Se 55	cca gtc atc atg aad Pro Val Ile Met Asi 10  gg ttc cca ggc ttt or p Phe Pro Gly Phe 30  gt ttt cca ttc tgt or er Phe Pro Phe Cys or 45  gc ccg cct gtg ctg ar er Pro Pro Val Leu 26 60  cc tac gcc atc gtc or	c caa agg 49 n Gln Arg 15 cct gta 97 Pro Val  ggc acc 145 Gly Thr agg ctg 193 Arg Leu gga acc 241
<220> <221> CDS <222> (2)(487) <223> Product = olface <400> 193 t gtg gcc atc tgt agt    Val Ala Ile Cys Ser    1	tory receptor  ccc ttg cac tac Pro Leu His Tyr  t gct gcc tcc tc a Ala Ala Ser Tr 25 a tgg ctc ttc ac r Trp Leu Phe Se 40 c ttc tgt gac ac e Phe Cys Asp Se 55 a ctg ttt gag at a Leu Phe Glu Il	cca gtc atc atg aad Pro Val Ile Met Asi 10  gg ttc cca ggc ttt or p Phe Pro Gly Phe 30  gt ttt cca ttc tgt or er Phe Pro Phe Cys or 45  gc ccg cct gtg ctg ar er Pro Pro Val Leu ar 60  cc tac gcc atc gtc or er Tyr Ala Ile Val or 75  cg atc ttg tgt tcc or eu Ile Leu Cys Ser 3	c caa agg 49 n Gln Arg 15 cct gta 97 Pro Val  ggc acc 145 Gly Thr agg ctg 193 Arg Leu  gga acc 241 Gly Thr 80 tat act 289

aaa Lys	gcc Ala	ttc Phe 115	tct Ser	acg Thr	tgt Cys	tcc Ser	tca Ser 120	cac His	ctc Leu	ctt Leu	gtt Val	gtc Val 125	tct Ser	ctt Leu	ttc Phe	385
tat Tyr	ata Ile 130	tca Ser	tta Leu	agc Ser	ctc Leu	aca Thr 135	tat Tyr	ttt Phe	cgg Arg	cct Pro	aaa Lys 140	tca Ser	aat Asn	aat Asn	tct Ser	433
cct Pro 145	gag Glu	ggc Gly	aag Lys	aag Lys	ctg Leu 150	cta Leu	tca Ser	ttg Leu	tcc Ser	tac Tyr 155	act Thr	gtt Val	gtg Val	act Thr	ccc Pro 160	481
atg Met	_															487
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<211> 162 <212> PRT

<213> Hylobates lar

<220>

<221> misc\_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA124; Accession DDBJ/EMBL/GenBank = AF179741

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Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg

Thr Arg Ala Lys Leu Ala Ala Ser Trp Phe Pro Gly Phe Pro Val

Ala Thr Val Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr

Asn Lys Val Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu 50 55

Val Cys Ala Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr

Ile Leu Val Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr

His Ile Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe

Tyr Ile Ser Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser 130 135 140

## Pro Glu Gly Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro 145 150 160 Met Leu

<210> 195

<211> 487

<212> DNA <213> Hylobates lar

<220>

<221> misc\_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA125; Accession DDBJ/EMBL/GenBank = AF179742

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<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 195

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Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg
1 5 10 15

gtc tgc ata ctg ctt gtt ttt act tct tgg ctg att tca ttc tta atc

Val Cys Ile Leu Leu Val Phe Thr Ser Trp Leu Ile Ser Phe Leu Ile

20 25 30

ata ttc cct gca ctc atg ttg ctc tta aag ctt gat tac tgt agg tct 145

Ile Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Arg Ser

35 40 45

aat att att gac cat ttt acc tgt gat tat ttt ccc ctg ctg caa ctt 193
Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
50 55 60

gct tgt tca gac aca aaa ttc tta gag gtg atg gca ttt tct tgt gct 241 Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Ala Phe Ser Cys Ala 65 70 75 80

gtg ttt act cta atg ttc act ttg gca tta ata tct ctg tcc tac ata 289
Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Ser Leu Ser Tyr Ile
85 90 95

tac att atc aga aca att ttg aga att cct tct act agt cag agg aca

Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr

100 105 110

aag gcc ttt tcc aca tgt tct tcc cac atg gtt gtt att tcc atc tct
Lys Ala Phe Ser Thr Cys Ser Ser His Met Val Val Ile Ser Ile Ser
115 120 125

tat ggc agc tgc att ttt atg tac att aaa ccc tca gca aaa gat aga
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
130 135 140

gtg tcc ttg agc aag gga gtg gca ata cta aac acc tca gta gcc ccc Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro 155 160

atg atg 487 Met Met

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<210> 196
<211> 162
<212> PRT
<213> Hylobates lar
<220>
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<222> (1)..(487)
<223> Taxon = 9580; gene = HLA125; Accession DDBJ/EMBL/GenBank = AF179742
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Val Cys Ile Leu Leu Val Phe Thr Ser Trp Leu Ile Ser Phe Leu Ile
Ile Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Arg Ser
Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Ala Phe Ser Cys Ala
Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Ser Leu Ser Tyr Ile
                                     90
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
            100
                                 105
Lys Ala Phe Ser Thr Cys Ser Ser His Met Val Val Ile Ser Ile Ser
        115
                             120
                                                  125
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
Met Met
<210> 197
<211> 484
<212> DNA
<213> Hylobates lar
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<222> (1)..(484)
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       (2)..(484)
<222>
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                                                                         49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
ctc tgt gtc ttc tta gtg gct ata tct tgg att ctg tct tgt gcc agc
                                                                         97
Leu Cys Val Phe Leu Val Ala Ile Ser Trp Ile Leu Ser Cys Ala Ser
tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg
                                                                        145
Ser Leu Ser His Thr Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
        35
                             40
aac acc atc ccc cac gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg
                                                                        193
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
                                                                        241
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc
                                                                        289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                85
                                     90
tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac
                                                                        337
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
            100
                                 105
aaa geg tee acg tgt gge tee cat ett tet gtg gtg tet ete tat tat
                                                                        385
Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
                             120
ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att
                                                                        433
Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg
                                                                        481
Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
                    150
                                         155
ttg
                                                                        484
Leu
<210> 198
<211> 161
<212> PRT
<213> Hylobates lar
<220>
<221>
      misc_feature
<222>
       (1)..(484)
       Taxon = 9580; gene = HLA126; Accession DDBJ/EMBL/GenBank = AF179743
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
```

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Leu Cys Val Phe Leu Val Ala Ile Ser Trp Ile Leu Ser Cys Ala Ser
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
        35
                             40
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                                     90
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
                                 105
Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
                            120
Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
145
                    150
                                         155
Leu
<210> 199
<211> 487
<212> DNA
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9580; gene = HLA127; Accession DDBJ/EMBL/GenBank = AF179744
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 199
t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc
                                                                       49
  Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
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cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys

25

gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac 145 Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40 45	
cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg 193 His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60	
tcc tgc tca gat acc tcc ctc aat cag ttg gca atc ttt aca gca gga 241 Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80	
ttg aca gcc att atg ctt cca ttc ttg tgc atc ctg gtt tct tat ggt 289 Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95	
cac att ggg gtc acc atc ctc cag att ccc tct acc aag ggc ata tgc 337 His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100 105 110	
aaa gcc ttg tcc att tgt gga tcc cac ctc tca gtg gtg act atc tat 385 Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125	
tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc  Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr  130 135 140	
aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 155 160	
atg ttg Met Leu	
<210> 200 <211> 162 <212> PRT <213> Hylobates lar	
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<pre>&lt;400&gt; 200 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser 1</pre>	
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30	
Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40 45	
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60	
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80	

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Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                                 90
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
            100
                                 105
                                                     110
Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
                             120
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                                        155
Met Leu
<210> 201
<211> 484
<212> DNA
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(484)
       Taxon = 9580; gene = HLA128; Accession DDBJ/EMBL/GenBank = AF179745
<220>
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<222>
       (2)..(484)
<223> Product = olfactory receptor
<400> 201
t gtt gcc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag
                                                                       49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
                                      10
ctc tgt gtc ttc tta gtg gct gta tct tgg att ctg tct tgt gcc agc
                                                                       97
Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
            20
                                25
tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg
                                                                      145
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
aac acc atc ccc cac gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg
                                                                      193
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
    50
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg
                                                                      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
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289

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac  Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His  100 105 110
aaa gcg tcc acg tgt ggc tcc cat ctt tct gtg gtg tct ctc tat tat  Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr  115 120 125
ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ile 130 135 140
gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg  Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met  145 150 155 160
ttg Leu
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Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80
Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His 100 105 110
Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120 125
Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile 130 135 140

Asp	гàг	Asp	vaı	TTE	۷aı	Ala	Val	Met	Tyr	Thr	Val	Ile	Thr	Pro	Met
145					150					155					160

Leu

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cag Gln	tgt Cys	gtc Val	atg Met 20	ctg Leu	gtg Val	gct Ala	Gly 999	tcc Ser 25	tgg Trp	gtc Val	atc Ile	gct Ala	tgt Cys 30	gcg Ala	tgt Cys	97
gct Ala	ctt Leu	ttg Leu 35	cat His	acc Thr	ctc Leu	ctc Leu	ctg Leu 40	gcc Ala	cag Gln	ctt Leu	tcc Ser	ttt Phe 45	tgt Cys	gct Ala	gac Asp	145
cac His	atc Ile 50	atc Ile	cct Pro	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ttg Leu	193
tcc Ser 65	tgc Cys	tca Ser	gat Asp	acc Thr	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttc Phe	aca Thr	gta Val	80 GJÀ aaa	241
gtg Val	gtg Val	gtc Val	att Ile	acc Thr 85	ctg Leu	cca Pro	ttc Phe	atg Met	tgt Cys 90	atc Ile	ctg Leu	gta Val	tca Ser	tat Tyr 95	ggc Gly	289
tac Tyr	att Ile	Gly aaa	gcc Ala 100	acc Thr	atc Ile	ctg Leu	agg Arg	gtc Val 105	cct Pro	tca Ser	acc Thr	aaa Lys	999 Gly 110	atc Ile	cac His	337
aaa Lys	gcg Ala	tcc Ser 115	acg Thr	tgt Cys	ggc Gly	tcc Ser	cat His 120	ctt Leu	tct Ser	gtg Val	gtg Val	tct Ser 125	ctc Leu	tat Tyr	tat Tyr	385
Gly aaa	tca Ser 130	ata Ile	ttt Phe	ggc Gly	cag Gln	tac Tyr 135	ctt Leu	ttc Phe	ccg Pro	acc Thr	gca Ala 140	agc Ser	agt Ser	tcc Ser	att Ile	433
gac Asp 145	aag Lys	gat Asp	gtc Val	att Ile	gtg Val 150	gct Ala	gtc Val	atg Met	tac Tyr	aca Thr 155	gtg Val	atc Ile	aca Thr	ccc Pro	atg Met 160	481

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<222> (1)...(484)

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Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 55

Ser Cys Ser Asp Thr Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His

Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120

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Leu

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<211> 486

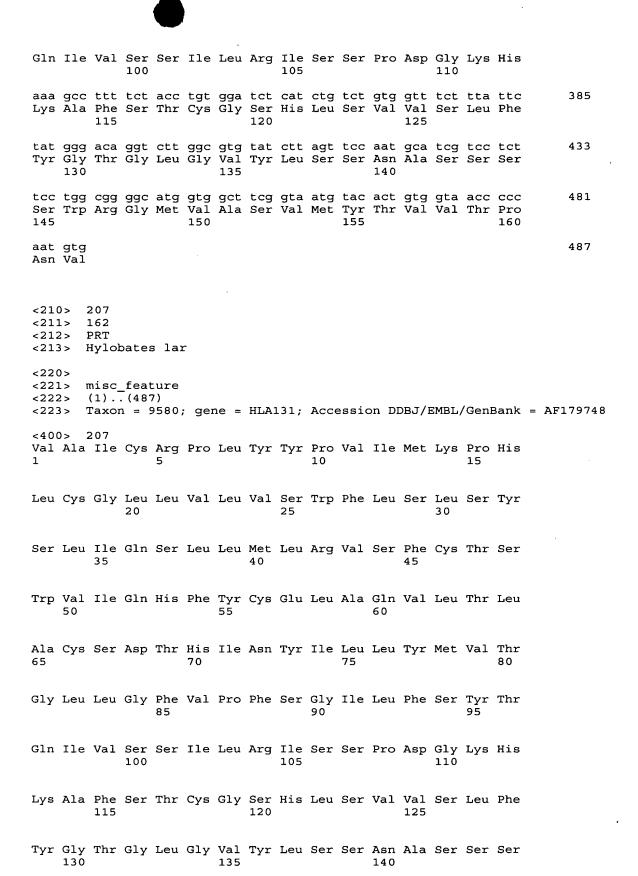
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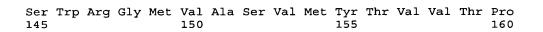
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                                                                      120
geocagettt cettttgtge tgaccacate ateceteaet tettetgtga cettggtgee
                                                                      180
ctgctcaagt tgtcctgctc agatacctcc ctcaatcagt tggcaatctt tacagcagga
                                                                      240
ttgacageca ttatgettee attettgtge atcetggttt ettatggtea eattggggte
                                                                      300
                                                                      360
accatectee agatteeete taccaaggge atatgeaaag eettgteeat ttgtggatee
caceteteag tggtgactat ctattatggg acaattattg gtetetattt tetteececa
                                                                      420
tccagcaaca ccaatgacaa gaacataatt gcttcagtga tatacacagt agtcactccc
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atgttg
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  Val Ala Ile Cys Arg Pro Leu Tyr Tyr Pro Val Ile Met Lys Pro His
                                      10
                                                           15
ctc tgt ggc ctg ctg gtt ctt gtg tcc tgg ttc ctc agc ttg tca tac
                                                                       97
Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr
            20
tcc ctg atc cag agt ctg ttg atg ctg cgg gtg tcc ttc tgc acc agt
                                                                      145
Ser Leu Ile Gln Ser Leu Leu Met Leu Arg Val Ser Phe Cys Thr Ser
tgg gtc att cag cac ttt tac tgt gag ctt gct cag gtc ctc acg ctt
                                                                      193
Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu
                        55
                                                                      241
gcc tgc tca gac aca cac atc aat tac atc ctg ctc tac atg gtg acc
Ala Cys Ser Asp Thr His Ile Asn Tyr Ile Leu Leu Tyr Met Val Thr
ggc ctt ttg ggc ttt gtg ccc ttc tca ggg atc ctt ttc tcc tac acc
                                                                      289
Gly Leu Leu Gly Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr
                85
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                                    90
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Asn Val

<211> 4 <212> D	208 187 DNA Hyloba	ites la	r											
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cag tgt Gln Cys	Val M	itg ctg let Leu :0	gtg Val	gct Ala	Gly ggg	tcc Ser 25	tgg Trp	gtc Val	atc Ile	gct Ala	tgt Cys 30	gcg Ala	tgt Cys	97
gct ctt Ala Leu														145
cac atc His Ile 50														193
tcc tgc Ser Cys 65														241
ttg aca Leu Thr														289
cac att His Ile	Gly V													337
aaa gcc Lys Ala	Leu S	er Ile	tgt Cys	Gly	Ser	His	Leu	Ser	Val	Val	Thr	atc Ile	tat Tyr	385
tat ggg Tyr Gly 130														433
aat gac Asn Asp 145														481
atg ttg														487

## Met Leu

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Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 90

His Ile Gly Val Thr Ile Leu Gln Thr Pro Ser Thr Lys Gly Ile Cys

Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 120

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Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 150 155

Met Leu

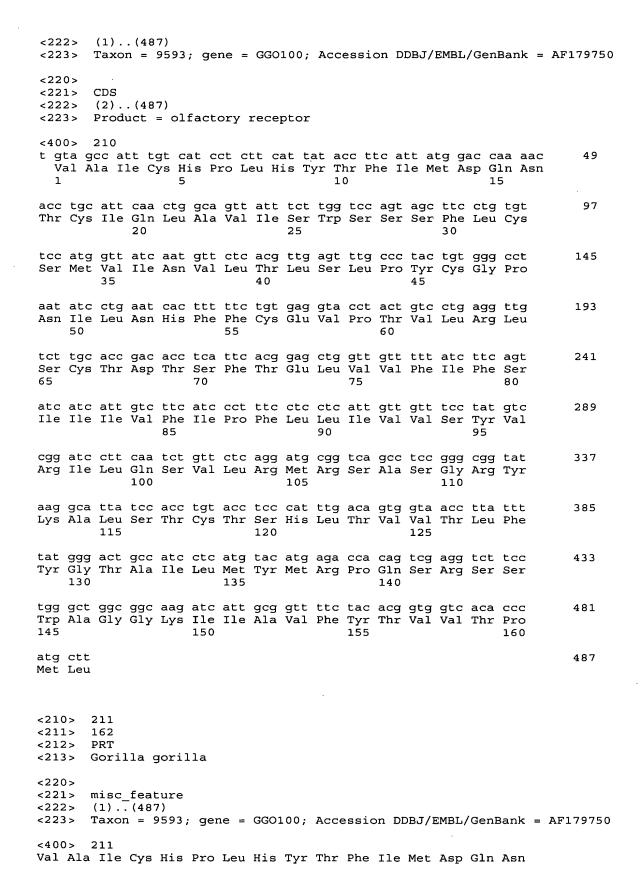
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<211> 487 <212> DNA

<213> Gorilla gorilla

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1				5					10					15		
Thr	Сув	Ile	Gln 20	Leu	Ala	Val	Ile	Ser 25	Trp	Ser	Ser	Ser	Phe 30	Leu	Cys	
Ser	Met	Val 35	Ile	Asn	Val	Leu	Thr 40	Leu	Ser	Leu	Pro	Tyr 45	Cys	Gly	Pro	
Asn	Ile 50	Leu	Asn	His	Phe	Phe 55	Cys	Glu	Val	Pro	Thr 60	Val	Leu	Arg	Leu	
Ser 65	Cys	Thr	Asp	Thr	Ser 70	Phe	Thr	Glu	Leu	Val 75	Val	Phe	Ile	Phe	Ser 80	
Ile	Ile	Ile	Val	Phe 85	Ile	Pro	Phe	Leu	Leu 90	Ile	Val	Val	Ser	Tyr 95	Val	
Arg	Ile	Leu	Gln 100	Ser	Val	Leu	Arg	Met 105	Arg	Ser	Ala	Ser	Gly 110	Arg	Tyr	
Lys	Ala	Leu 115	Ser	Thr	Cys	Thr	Ser 120	His	Leu	Thr	Val	Val 125	Thr	Leu	Phe	
Tyr	Gly 130	Thr	Ala	Ile	Leu	Met 135	Tyr	Met	Arg	Pro	Gln 140	Ser	Arg	Ser	Ser	
Trp 145	Ala	Gly	Gly	Lys	Ile 150	Ile	Ala	Val	Phe	Tyr 155	Thr	Val	Val	Thr	Pro 160	
Met	Leu															
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<40 tgt		212 att a	agcca	accca	ac tt	cact	catco	c cat	ccto	catg	aato	cagag	ggg t	ctgt	ctcca	60

120

360

gattaccggg agctcctggg cctttgggat aatcgatggc tttgatccag atggtggtag

180 taatgaattt cccctactgt ggcttgagga aggtgaacca tttcttctgt gagatgctat

ccttgttgaa gctggcctgt gtagacacat ccctgtttga gaaggtgata tttgcttgct 240

300 gtgtcttcat gcttctctc ccattctcca tcatcgtggc ctcctatgct cgcattctag

ggactgtgct gcaaatgcac tctgctcagg cctggaaaaa ggccctggcc acctgctcct

	cacc	cyac	age	tgte	acc	CECE	tcta	tg g	ggca	gcca	t gt	tcat	ctac	ctg	aggccta	420	
gg	gct	accg	ggc	cccc	agc	catg	acaa	gg t	ggcc	tcta	t ct	tcta	caca	gtc	cttacto	480	
CC	atgo	tg														488	
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ttc Phe	tgt Cys	gto Val	ttc Phe 20	tta Leu	gtg Val	gct Ala	gta Val	tct Ser 25	tgg Trp	att Ile	ctg Leu	tct Ser	tgt Cys 30	gcc Ala	agc Ser	97	
tcc Ser	ctc Leu	tct Ser 35	cac His	acc Thr	gtt Val	ctc Leu	ctg Leu 40	acc Thr	cag Gln	ctg Leu	tct Ser	ttc Phe 45	tgt Cys	gct Ala	gcg Ala	145	
aac Asn	acc Thr 50	atc Ile	ccc Pro	cat His	gtc Val	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	gct Ala	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu	193	
tcc Ser 65	tgc Cys	tca Ser	gat Asp	atc Ile	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttc Phe	aca Thr	gta Val	80 GJA 333	241	
gtg Val	gtg Val	gtc Val	att Ile	acc Thr 85	ctg Leu	cca Pro	ttc Phe	atg Met	tgt Cys 90	atc Ile	ctg Leu	gta Val	tca Ser	tat Tyr 95	ggt Gly	289	
tac Tyr	att Ile	gl <sup>à</sup> aaa	gcc Ala 100	acc Thr	atc Ile	ctg Leu	gly aaa	gtc Val 105	cct Pro	tca Ser	acc Thr	aaa Lys	999 Gly 110	atc Ile	cac His	337	
aaa Lys	gca Ala	ttg Leu 115	tcc Ser	aca Thr	tgt Cys	ggc Gly	tcc Ser 120	cat His	ctc Leu	tct Ser	gtg Val	gtg Val 125	tct Ser	ctc Leu	tat Tyr	385	
at Tyr	999 Gly 130	tca Ser	ata Ile	ttt Phe	ggc Gly	cag Gln 135	tac Tyr	ctt Leu	ttc Phe	ccg Pro	act Thr 140	gta Val	agc Ser	agt Ser	ttt Phe	433	
itt [le [45	gac Asp	aag Lys	gat Asp	gtc Val	att Ile 150	gtg Val	gct Ala	ctc Leu	atg Met	tac Tyr 155	acg Thr	gtg Val	gtc Val	aca Thr	ccc Pro 160	481	
icg 'hr	ttg															487	

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Phe Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
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Ser Leu Ser His Thr Val Leu Leu Thr Gln Leu Ser Phe Cys Ala Ala
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                                    90
Tyr Ile Gly Ala Thr Ile Leu Gly Val Pro Ser Thr Lys Gly Ile His
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Phe
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Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
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Thr Leu
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                                                                     120
cctgagcttc ccatattgcg gtgcacacga gategatcac ttcttctgcg aggccccgt
                                                                     180
gctggttcat ttggcttgtg ctgacacttc agtcttcgaa aacgccatgt acatctgctg
                                                                     240
tgtgttaatg ctcctggtcc ccttttccct catcctgtcc tcctatggtc tcatcctcgc
                                                                     300
tgctgttctg cacatgcgct ctacagaagc ccgcaagaag gcctttgcca cctgctcttc
                                                                     360
acatttggct gtggtgggac tcttttatgg agctgccatt tttacctata tgagacccaa
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atcccacagg tccactaacc acgataaggt tgtgtcagcc ttctatagta tgttcacccc
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tttactaa
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= AF179754
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teatecetea ettettetgt gacettggtg ceetgeteaa gttgteetge teagacacet
                                                                     180
ccctcaatca gttagcaatc tttacagcag gattgacagc cattatgctt ccattcctgt
                                                                     240
gcatcctggt ttcttatggt cacattgggg tcaccatcct ccagattccc tctaccaagg
                                                                     300
                                                                     360
gcatatgcaa agccttgtcc acttgtggat cccacctctc agtggtgact atctattatg
ggacaattat tggtctctat tttcttcccc catcctgcaa caccaatgac gagaacataa
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gtg tgt gtt gtg ctg ctg gta atg tcc tgg gtt gga gga ttt ctg cac
Val Cys Val Val Leu Leu Val Met Ser Trp Val Gly Gly Phe Leu His
                                                                          97
             20
 tca gta ttt caa ctt agc att att tat ggg ctc cca ttc tgt ggc ccc
                                                                         145
Ser Val Phe Gln Leu Ser Ile Ile Tyr Gly Leu Pro Phe Cys Gly Pro
aat gtc att gat cac ttt ttc tgt gac atg tat ccc tta ttg aaa ctg
                                                                         193
Asn Val Ile Asp His Phe Phe Cys Asp Met Tyr Pro Leu Leu Lys Leu
                         55
gtc tgc act gac acc cat gtt att ggc ctc tta gtg gtg acc aat gga
                                                                         241
Val Cys Thr Asp Thr His Val Ile Gly Leu Leu Val Val Thr Asn Gly
                     70
gga ctg tct tgc act att gtg ttt ctg ctc tta ctc atc tct tat ggt
                                                                         289
Gly Leu Ser Cys Thr Ile Val Phe Leu Leu Leu Leu Ile Ser Tyr Gly
                 85
gtc atc ttg cac tct cta aag aaa ctt agt cag aaa ggg agg caa aaa
                                                                         337
Val Ile Leu His Ser Leu Lys Lys Leu Ser Gln Lys Gly Arg Gln Lys
             100
ged etc tea ace tge agt tee eac atc act gtg gtt gte tte ttt
                                                                         385
Ala Leu Ser Thr Cys Ser Ser His Ile Thr Val Val Val Phe Phe
                             120
gtt cct tgt att ttt atg tat gct aga cct gct agg agc ttc ccc att
                                                                         433
Val Pro Cys Ile Phe Met Tyr Ala Arg Pro Ala Arg Ser Phe Pro Ile
                         135
gac aaa tca gtg agt gtg ttt tat aca gtc ata acc cca atg ct
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Asp Lys Ser Val Ser Val Phe Tyr Thr Val Ile Thr Pro Met
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Val Cys Val Val Leu Leu Val Met Ser Trp Val Gly Gly Phe Leu His
            2.0
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Ser Val Phe Gln Leu Ser Ile Ile Tyr Gly Leu Pro Phe Cys Gly Pro

35

ASII	50 50	116	Asp	nis	PHE	55	Cys	Asp	Mec	ıyı	60	ьeu	ьeu	гуѕ	ьeu	
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Gly	Leu	Ser	Cys	Thr 85	Ile	Val	Phe	Leu	Leu 90	Leu	Leu	Ile	Ser	Tyr 95	Gly	
Val	Ile	Leu	His 100	Ser	Leu	Lys	Lys	Leu 105	Ser	Gln	Lys	Gly	Arg 110	Gln	Lys	
Ala	Leu	Ser 115	Thr	Cys	Ser	Ser	His 120	Ile	Thr	Val	Val	Val 125	Phe	Phe	Phe	
Val	Pro 130	Cys	Ile	Phe	Met	Tyr 135	Ala	Arg	Pro	Ala	Arg 140	Ser	Phe	Pro	Ile	
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	gcc Ala 50															193
	tgc Cys															241

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tac atc atc agc acc atc ctc agg atc ccc tct gcc agt ggc cgg agc Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser 100 105 110	337
aaa gcc ttc tcc acg tgc tcc tcg cat ctc acc gtg gtg ctc att tgg Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp 115 120 125	385
tat ggg tcc aca att ttc ctt cac gtc cgc acc tct atc aaa gac gcc Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala 130 135 140	133
ttg gat ctg atc aaa gct gtc cac gtc ctg aac act gtg gtg act cca Leu Asp Leu Ile Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro 145 150 155 160	181
gtt tta a Val Leu	188
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Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp

115 120 125

Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala 130 135 140

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Val Leu

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420

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	20			25		30	
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cac His	atc Ile 50	atc Ile	cct Pro	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ttg Leu		193
tcc Ser 65	tgc Cys	tca Ser	gac Asp	acc Thr	tcc Ser 70	ctc Leu	aat Asn	cag Gln	tta Leu	gca Ala 75	atc Ile	ttt Phe	aca Thr	gca Ala	gga Gly 80		241
ttg Leu	aca Thr	gcc Ala	att Ile	atg Met 85	ctt Leu	cca Pro	ttc Phe	ctg Leu	tgc Cys 90	atc Ile	ctg Leu	gtt Val	tct Ser	tat Tyr 95	ggt Gly		289
cac His	att Ile	gly aaa	gtc Val 100	acc Thr	atc Ile	ctc Leu	cag Gln	att Ile 105	ccc Pro	tct Ser	acc Thr	aag Lys	ggc Gly 110	ata Ile	tgc Cys		337
aaa Lys	gcc Ala	ttg Leu 115	tcc Ser	act Thr	tgt Cys	gga Gly	tcc Ser 120	cac His	ctc Leu	tca Ser	gtg Val	gtg Val 125	act Thr	atc Ile	tat Tyr		385
tat Tyr	999 Gly 130	aca Thr	att Ile	att Ile	ggt Gly	ctc Leu 135	tat Tyr	ttt Phe	ctt Leu	ccc Pro	cca Pro 140	tcc Ser	agc Ser	aac Asn	acc Thr		433
aat Asn 145	gac Asp	aag Lys	aac Asn	ata Ile	att Ile 150	gct Ala	tca Ser	gtg Val	ata Ile	tac Tyr 155	aca Thr	gta Val	gtc Val	act Thr	ccc Pro 160		481
atg Met	_															•	187
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His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu

Ser 65	Cys	Ser	qaA	Thr	Ser 70	Leu	Asn	Gln	Leu	Ala 75	Ile	Phe	Thr	Ala	80 81y	
Leu	Thr	Ala	Ile	Met 85	Leu	Pro	Phe	Leu	Сув 90	Ile	Leu	Val	Ser	Tyr 95	Gly	
His	Ile	Gly	Val 100	Thr	Ile	Leu	Gln	Ile 105	Pro	Ser	Thr	Lys	Gly 110	Ile	Cys	
Lys	Ala	Leu 115	Ser	Thr	Cys	Gly	Ser 120	His	Leu	Ser	Val	Val 125	Thr	Ile	Tyr	
Tyr	Gly 130	Thr	Ile	Ile	Gly	Leu 135	Tyr	Phe	Leu	Pro	Pro 140	Ser	Ser	Asn	Thr	
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cct Pro	ctg Leu	gtt Val 35	cat His	gtg Val	agt Ser	tta Leu	cta Leu 40	ttg Leu	cga Arg	cta Leu	act Thr	ttc Phe 45	tgc Cys	agg Arg	ttt Phe	145
aac Asn	ata Ile 50	ata :Ile	cat His	tat Tyr	ttc Phe	tac Tyr 55	tgt Cys	gaa Glu	att Ile	tta Leu	caa Gln 60	ctg Leu	ttc Phe	aaa Lys	att Ile	193
tca Ser 65	tgc Cys	aat Asn	ggt Gly	cca Pro	tct Ser 70	att Ile	aac Asn	gca Ala	cta Leu	ata Ile 75	ata :Ile	ttt Phe	att Ile	ttt Phe	ggt Gly 80	241
					000	act	++=	ato	act	ato	ata	ato	tat	tat	act	289

Ala File 1	le Gln	Ile 85	Pro	Thr	Leu	Met	Thr 90	Ile	Ile	Ile	Ser	Tyr 95	Thr	
cgt gtg c Arg Val L	etc ttt seu Phe 100	gat Asp	att Ile	ctg Leu	aaa Lys	aaa Lys 105	aag Lys	tct Ser	gaa Glu	aag Lys	ggc Gly 110	aga Arg	agc Ser	337
aaa gcc t Lys Ala P 1	tc tcc he Ser 15	aca Thr	tgc Cys	ggc Gly	gcc Ala 120	cat His	ctg Leu	ctt Leu	tct Ser	gtc Val 125	tca Ser	ttg Leu	tac Tyr	385
tac gga a Tyr Gly T 130	act ctg Chr Leu	atc Ile	ttc Phe	atg Met 135	tat Tyr	gtg Val	cgt Arg	cct Pro	gca Ala 140	tct Ser	ggc Gly	tta Leu	gct Ala	433
gaa gac c Glu Asp G 145	aa gac Sln Asp	aaa Lys	gtg Val 150	tat Tyr	tct Ser	ctg Leu	ttt Phe	tac Tyr 155	acg Thr	att Ile	ata Ile	att Ile	ccc Pro 160	481
ctg cta Leu Leu														487
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Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala 130 135 140

Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro 145 150 155 160

Leu Leu

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cc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg er Leu Ser His Thr Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45
ac acc gtc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg 193 sn Thr Val Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60
cc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg 241 er Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 75 80
tg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc 289 al Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95
ac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac 337 yr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His 100 105 110
aa gca ttg tcc aca tgt ggc tcc cat ctc tct gtg gtg tct ctc tat 385 ys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 115 120 125
at ggg tca ata ttt ggc cag tac ctt ttc ccg act gta agc agt tct 433 yr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 140

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atg Met	_																487
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Ser	Leu	Ser 35	His	Thr	Leu	Leu	Leu 40	Thr	Arg	Leu	Ser	Phe 45	Cys	Ala	Ala		
Asn	Thr 50	Val	Pro	His	Val	Phe 55	Cys	Asp	Leu	Ala	Ala 60	Leu	Leu	Lys	Leu		
Ser 65	Cys	Ser	Asp	Ile	Phe 70	Leu	Asn	Glu	Leu	Val 75	Met	Phe	Thr	Val	Gly 80		
Val	Val	Val	Ile	Thr 85	Leu	Pro	Phe	Met	Cys 90	Ile	Leu	Val	Ser	Tyr 95	Gly		
Tyr	Ile	Gly	Ala 100	Thr	Ile	Leu	Arg	Val 105	Pro	Ser	Thr	Lys	Gly 110	Ile	His		
Lys	Ala	Leu 115	Ser	Thr	Cys	Gly	Ser 120	His	Leu	Ser	Val	Val 125	Ser	Leu	Tyr		
Tyr	Gly 130	Ser	Ile	Phe	Gly	Gln 135	Tyr	Leu	Phe	Pro	Thr 140	Val	Ser	Ser	Ser		
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Met Leu

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Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                                                                          97
            20
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac
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Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
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Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
                         55
qcc ttc tct qac act cga gtt aat gaa tgg gtg ata ttt atc atg gga
                                                                         241
Ala Phe Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
ggg ctc att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca
                                                                         289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                 85
aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc
                                                                         337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
            100
aag gcc ctc tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc
                                                                         385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
                             120
                                                  125
                                                                         433
tat gga acc gtt att ggt ctc tac tta tgc tca tca gct aat agt tct
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser
act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc
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Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
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Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
Ala Phe Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
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Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
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Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser
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Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
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                                                                       120
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                                                                      240
ttttctggtc atcacaacca gcatttcagt gattcttaca tcgtacttgt tcatcattca
                                                                      300
gtctattctg aagattcgta cagcaggtgg aaagccaaga ccttctccac ctgtgcttct
                                                                      360
cacaagactg cattgactct cttctttgga acactcatat tcatatacct gaaaggcaac
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ggtgaaactg tctttctgtg ggccaaatgt catcagtcac ttcttctgtg atcttccccc
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actgttgaag ctgtcatgtt ctgagacatc tatgaatgaa ttgttgcttt tgatcttctc
                                                                      240
                                                                      300
tggcattatt gccacgctca cttttttgac tgtggtgatc tcctacatct tcattgttgc
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ctc Leu	tgc a Cys T	act Thr	cta Leu 20	ctt Leu	gtg Val	ctg Leu	tgt Cys	gcc Ala 25	tgg Trp	cta Leu	agt Ser	gly ggg	ttt Phe 30	ctg Leu	acc Thr	97
att Ile	ttc o	cca Pro 35	ccc Pro	ctt Leu	atg Met	ctt Leu	ctc Leu 40	ctc Leu	cag Gln	ctg Leu	gat Asp	tac Tyr 45	tgt Cys	gct Ala	tcc Ser	145
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tct Ser 65	tgt (	tca Ser	gat Asp	aca Thr	tgg Trp 70	ctc Leu	cta Leu	gaa Glu	gta Val	att Ile 75	ggt Gly	ttt Phe	tac Tyr	ttt Phe	gct Ala 80	241
ttg Leu	gtt a Val '	act Thr	ttg Leu	ctg Leu 85	ttc Phe	act Thr	ttg Leu	gca Ala	tta Leu 90	gtg Val	att Ile	tta Leu	tct Ser	tac Tyr 95	atg Met	289
tac Tyr	att i	atc Ile	agg Arg 100	acc Thr	att Ile	ttg Leu	aga Arg	atc Ile 105	ccg Pro	tct Ser	gcc Ala	agt Ser	caa Gln 110	aga Arg	aaa Lys	337
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gca Ala 145	tca Ser	ttg Leu	aca Thr	aaa Lys	gga Gly 150	ata Ile	gct Ala	att Ile	ctc Leu	aat Asn 155	aca Thr	tct Ser	gtt Val	gcc Ala	ccc Pro 160	481
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Asn Val Ile Asp His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu
Ser Cys Ser Asp Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala
Leu Val Thr Leu Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys
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Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
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Tyr Gly Ser Cys Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys
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Met Leu
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Leu Cys Ala Leu Met Leu Ala Met Cys Trp Leu Leu Thr Asn Cys Pro
gca ttg atg cac acg ctg ttg ctg acc cgt gtg gct ttc tgt gcc cag
                                                                         145
Ala Leu Met His Thr Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln
agg gec atc eec cac tte tac tgt gat eec agt get etc etg aag etc
                                                                         193
Arg Ala Ile Pro His Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu
gcc tgc tcg gat acc cgc ata aac gag ctg atg atc atc gcc atg ggc
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Ala Cys Ser Asp Thr Arg Ile Asn Glu Leu Met Ile Ile Ala Met Gly
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Leu Ala Phe Leu Thr Val Pro Leu Thr Leu Ile Val Phe Ser Tyr Val
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                                      90
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Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Leu Leu Phe
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Tyr Gly Ser Leu Met Gly Val Tyr Leu Leu Pro Pro Ser Ser Tyr Ser
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Arg Ala Ile Pro His Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu

Ala Cys Ser Asp Thr Arg Ile Asn Glu Leu Met Ile Ile Ala Met Gly 70

Leu Ala Phe Leu Thr Val Pro Leu Thr Leu Ile Val Phe Ser Tyr Val

Arg Ile Ser Trp Ala Val Leu Gly Ile Ser Ser Pro Gly Gly Arg Cys 105

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Leu Leu Phe 125

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tottg	485
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cac atc atg cac acc atc ctc agg atc cct tct gct ggg ggc aag cac His Ile Met His Thr Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys His 100 105 110	337
aaa gtc ttc tct acc tgt ggc tct cac ctg tca gtg gtc act ctc ttc Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe 115 120 125	385
tat ggg acc ctc ttt ctg gtg tat ttc cag cct tca tcc tcc tac tca Tyr Gly Thr Leu Phe Leu Val Tyr Phe Gln Pro Ser Ser Ser Tyr Ser 130 135 140	433
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Cys Cys Leu Met Leu Val Ala Ala Ser Trp Leu Cys Ser His Cys Leu
Ala Phe Ser Leu Thr Leu Leu Met Thr Gln Phe Ser Phe Cys Ala Ser
His Ser Ile Gln His Phe Phe Cys Asp Val Pro Pro Leu Leu Lys Leu
Ala Cys Ser Asp Thr His Ile Phe Gln Val Thr Met Leu Thr Glu Gly
Val Leu Ser Gly Val Ile Pro Leu Thr Cys Val Leu Val Ser Tyr Ala
His Ile Met His Thr Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys His
            100
Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe
                             120
        115
Tyr Gly Thr Leu Phe Leu Val Tyr Phe Gln Pro Ser Ser Ser Tyr Ser
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Ala Asp Thr Gly Met Val Ala Cys Val Val Tyr Thr Met Val Thr Pro
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Met Val
<210> 247
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<221> misc\_feature

<222> (1)(487) <223> Taxon = 13515; gene = EFU148; Accession DDBJ/EMBL/GenBank = AF179774
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gtc tgc aga aga ctt gtc ttt tgt tgt tgg gta gct ggt ctg ttt att 97 Val Cys Arg Arg Leu Val Phe Cys Cys Trp Val Ala Gly Leu Phe Ile 20 25 30
ata atc cct cca ctt agc ctg ggc cta aat ctg gaa ttt tgt gat tct 145 Ile Ile Pro Pro Leu Ser Leu Gly Leu Asn Leu Glu Phe Cys Asp Ser 35 40 45
gat acc att gat cat ttt atc tgt gat gca tct ccc ctc ctg aat atc 193 Asp Thr Ile Asp His Phe Ile Cys Asp Ala Ser Pro Leu Leu Asn Ile 50 55 60
tct tgt tca aat act tgg ttc atg gaa cag act gtt atc atc tgt gca 241 Ser Cys Ser Asn Thr Trp Phe Met Glu Gln Thr Val Ile Ile Cys Ala 65 70 75 80
gtg ctg acc ctc att atg aca ctt atg tgt gta gtt ctg tcc tac att 289 Val Leu Thr Leu Ile Met Thr Leu Met Cys Val Val Leu Ser Tyr Ile 85 90 95
tat atc atc aag aca att tta gga ttc tct tct gcc cag caa aag aaa 337 Tyr Ile Ile Lys Thr Ile Leu Gly Phe Ser Ser Ala Gln Gln Lys Lys 100 105 110
aaa gcc ttt tcc acc tgt tct tcc cac atg att gtg gtg tcc atc acc 385 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr 115 120 125
tat ggc agc tac atc ttc atc tat atc aaa cct tct gca aag gaa gaa 433 Tyr Gly Ser Tyr Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Glu 130 135 140
gta gcc att aac aag ggt gtg aca gtc ctc act act tcc atc gcc ccc 481 Val Ala Ile Asn Lys Gly Val Thr Val Leu Thr Thr Ser Ile Ala Pro 145 150 155 160
atg ctg Met Leu
<210> 248 <211> 162 <212> PRT <213> Eulemur fulvus
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<400> 248

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Ile Ile Pro Pro Leu Ser Leu Gly Leu Asn Leu Glu Phe Cys Asp Ser

Asp Thr Ile Asp His Phe Ile Cys Asp Ala Ser Pro Leu Leu Asn Ile

Ser Cys Ser Asn Thr Trp Phe Met Glu Gln Thr Val Ile Ile Cys Ala 70

Val Leu Thr Leu Ile Met Thr Leu Met Cys Val Val Leu Ser Tyr Ile 90

Tyr Ile Ile Lys Thr Ile Leu Gly Phe Ser Ser Ala Gln Gln Lys Lys 100

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr 120 115

Tyr Gly Ser Tyr Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Glu 135

Val Ala Ile Asn Lys Gly Val Thr Val Leu Thr Thr Ser Ile Ala Pro 155

Met Leu

<210> 249 <211> 487

<212> DNA <213> Eulemur fulvus

<220>

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<222> (2)..(487)

<223> Product = olfactory receptor

<400> 249

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gtc tgc aca ctg ctc gtc ttt gcc tct tgg ctg gtt tca ttc tta atc 97 Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile

20 gta ttc cca gca ctc atg ttg ctc tta aag ctt gat tac tgt gga ttt 145 Val Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Gly Phe aat att att gac cat ttt acc tgt gat tat ttt ccc ctg ctg cag ctt 193 Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu 55 tcc tgt tca gat aca aaa ttc ctg gag ata atg ggg ttt tcc tgt gct 241 Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala gtg ttt act cta atg ttc act ttg gca tta ata ttt ctg tcc tac atg 289 Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met cac atc gtg aga acg att ttg aga att cct tct act agt cag agg aca 337 His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr 105 100 aag gcc ttt tct aca tgt tct tcc cac atg att gtc atc tcc atc tct 385 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser 120 433 tat ggc agc tgc att ttt atg tac att aag ccc tca gca aag gat aga Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg 135 140 gta tot ttg ago aag goa gtg got gtg cta atc acc tca gta got ccc 481 Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro 155 150 487 . atg ctc Met Leu <210> 250 <211> 162 <212> PRT <213> Eulemur fulvus <220> <221> misc\_feature (1)..(487) <222> Taxon = 13515; gene = EFU149; Accession DDBJ/EMBL/GenBank = AF179775 <223> <400> 250 Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg :5 Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile 20

Val Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Gly Phe

Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu





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Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala

Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met 90

His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr 105

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg 130

Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro 160

Met Leu

<210> 251

<211> 484

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc\_feature

<222> (1)..(484)

<223> Taxon = 13515; gene = EFU150; pseudogene; Accession DDBJ/EMBL/GenBank = AF179776

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<210> 252

<211> 487

<212> DNA

<213> Eulemur fulvus

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<222>
      (2)..(487)
      Product = olfactory receptor
<223>
<400> 252
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                                                                       49
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ctg gct aca cag ctg gcc ttg ggc tcc tgg gtc tgt ggt ttc ctg gcc
                                                                       97
Leu Ala Thr Gln Leu Ala Leu Gly Ser Trp Val Cys Gly Phe Leu Ala
            20
att gca gtg ctg acg gcc ctt atc agt ggc ctg tcc ttc tgt ggc gcc
                                                                      145
Ile Ala Val Leu Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Ala
                            40
                                                                      193
cgt gcc atc aac cac ttc ttc tgt gac att gca ccc tgg att gcc ctg
Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu
gcc tgc acc agc aca cag gca ata gag ctc gtg gcc ttt gtg att gct
                                                                      241
Ala Cys Thr Ser Thr Gln Ala Ile Glu Leu Val Ala Phe Val Ile Ala
                                         75
                    70
ttt gtg gtc atc ctg agt tca tgc ctc atc acc ctg gtc tcc tac gtg
                                                                      289
Phe Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val
                                                         95
                85
tac att atc agc acc atc ctc agg atc cca tct gcc agc ggc cgg agc
                                                                      337
Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser
                                 105
aaa gcc ttc tct acg tgc tcc tct cac ctc acc gtg gtg ctc atc tgg
                                                                      385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp
                             120
        115
tat ggg tcc acg att ttt ctt cat gtc cgc acc tcc atc aca gac gcc
                                                                       433
Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Thr Asp Ala
    130
                                                                       481
ttg gat ctg acc aaa gct gtc cat gtc ctg aac acc gtg gtg act cca
Leu Asp Leu Thr Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro
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                     150
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gtt cta
Val Leu
<210> 253
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Ile Ala Val Leu Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Ala 35 40 45

Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu 50 55 60

Ala Cys Thr Ser Thr Gln Ala Ile Glu Leu Val Ala Phe Val Ile Ala 65 70 75 80

Phe Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val

Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp 115 120 125

Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Thr Asp Ala 130 135 140

Leu Asp Leu Thr Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro 145 150 155

Val Leu

<210> 254

<211> 487

<212> DNA

<213> Eulemur fulvus

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<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 254

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Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg

1 5 10 15

gtc tgc aca ctg ctc gtc ttt gcc tct tgg ctg gtt tca ttc tta atc

97

Val Cys Th	r Leu Leu 20	Val Phe		Ser Trp 25	Leu	Val	Ser	Phe 30	Leu	Ile	
gta ttc co Val Phe Pr 35	o Ala Leu	atg ttg Met Leu	ctc t Leu L 40	ta aag Leu Lys	g ctt s Leu	gat Asp	tac Tyr 45	tgt Cys	gga Gly	ttt Phe	145
aat att at Asn Ile Il 50	t gac cat e Asp His	ttt acc Phe Thr 55	tgt g Cys A	gat tat Asp Tyr	ttt Phe	ccc Pro 60	ctg Leu	ctg Leu	cag Gln	ctt Leu	193
tcc tgt tc Ser Cys Se 65	a gat aca r Asp Thr	aaa tto Lys Phe 70	ctg g Leu G	gag ata Glu Ile	a atg e Met 75	gly aaa	ttt Phe	tcc Ser	tgt Cys	gct Ala 80	241
gtg ttt ac Val Phe Th	t cta atg ir Leu Met 85	ttc act Phe Thr	ttg g	gca tta Ala Lei 90	a ata ı Ile	ttt Phe	ctg Leu	tcc Ser	tac Tyr 95	atg Met	289
cac atc gt His Ile Va	g agg acg al Arg Thr 100	att tto	Arg I	att cci Ile Pro 105	tct Ser	act Thr	agt Ser	cag Gln 110	agg Arg	aca Thr	337
aag gcc tt Lys Ala Ph 13	ne Ser Thr	tgt tct Cys Sei	tcc o Ser F 120	cac ato	g att t Ile	gtc Val	atc Ile 125	tcc Ser	atc Ile	tct Ser	385
tat ggc ag Tyr Gly Se 130	gc tgc att er Cys Ile	ttt ato Phe Met	Tyr ]	att aag Ile Ly	g ccc s Pro	tca Ser 140	gca Ala	aaa Lys	gat Asp	aga Arg	433
gta tct tt Val Ser Lo 145	g agc aag eu Ser Lys	g gca gtg s Ala Val 150	g gct q Ala V	gtg ct. Val Le	a atc u Ile 155	acc Thr	tca Ser	gta Val	gct Ala	ccc Pro 160	481
atg ctc Met Leu											487
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J2225 (1	sc_featur )(487) xon = 135		= EFU	153; A	ccess	ion	DDBJ	/EMB	L/Ge	nBank =	AF179778
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Val Ala I 1	le Cys Ly 5	s Pro Le	u His '	Tyr Ar 10		Ile	Met	Asn	Arg 15	Arg	
Val Cys T	hr Leu Le 20	u Val Ph		Ser Tr 25	p Leu	ı Val	Ser	Phe 30	Leu	Ile	
Val Phe P	ro Ala Le 5	u Met Le	u Leu 40	Leu Ly	rs Lei	ı Asp	Tyr 45	Cys	Gly	Phe	
Asn Ile I 50	le Asp Hi	s Phe Th 55	r Cys	Asp Ty	r Phe	Pro 60	Leu	Leu	Glr	ı Leu	

Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala 65 70 75 80	
Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met 85 90 95	
His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr 100 105 110	
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser 115 120 125	
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg 130 135 140	
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Met Leu	
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ggc ttc atg ctc act cca atc acc atg acc ttc ccc tac tgc agg tcc  Gly Phe Met Leu Thr Pro Ile Thr Met Thr Phe Pro Tyr Cys Arg Ser  35 40 45	
cgg gag att cac cat tcc ttc tgc gaa gtc cct gct gta acg acg ctt 193 Arg Glu Ile His His Ser Phe Cys Glu Val Pro Ala Val Thr Thr Leu 50 55 60	
tcc tgc tca gac acc tca ctc tat gaa atg ctc atg tac ctg tgc tgt  Ser Cys Ser Asp Thr Ser Leu Tyr Glu Met Leu Met Tyr Leu Cys Cys  65 70 75 80	

gtc ctc atg ctc ctc att cct gtg aca gtc att tca agc tcc tat tca Val Leu Met Leu Leu Ile Pro Val Thr Val Ile Ser Ser Ser Tyr Ser 85 90 95	289
ttc att ctc ctc acc atc cac agg atg ggc tca gca gag ggc cgg aag Phe Ile Leu Leu Thr Ile His Arg Met Gly Ser Ala Glu Gly Arg Lys 100 105 110	337
aag gcc ttt gcc acc tgt tcc tcc cac atg acc gtg gtt atc ctc ttc Lys Ala Phe Ala Thr Cys Ser Ser His Met Thr Val Val Ile Leu Phe 115 120 125	385
tat ggg gcc gcc atc tac acc tac atg ctc ccc agc tcc tac cac act Tyr Gly Ala Ala Ile Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr 130 135 140	433
cct gag aag gac atg atg gtg tct gtc ttt tat acc atc cta act cct Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro 145 150 155 160	481
gtg cta a Val Leu	488
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Phe Ile Leu Leu Thr Ile His Arg Met Gly Ser Ala Glu Gly Arg Lys 100 105 110

115 120 125

Tyr Gly Ala Ala Ile Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr 130 140

Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro 145 150 155 160

Val Leu

<210> 258
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<213> Eulemur fulvus

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= AF179780

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<210> 259 <211> 486

<212> DNA <213> Eulemur fulvus

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<223> Taxon = 13515; gene = EFU156; pseudogene; Accession DDBJ/EMBL/GenBank = AF179781

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tttaaatcta aaattctgtg actctaacat gattgatcat tttggttgcg atgcatttcc 180
cctggtgaaa atctcatgct cagacacatg gttcatggaa cagacggtta tcatctgtgc 240

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tgtgctgacc ctgaatatga ctctaacttg tgtagttctg tcatacgctt acatcatcaa
                                                                     300
gacaattttt agatteeett etgteeagea aaggaaaaag geetttteea eetgttette
                                                                     360
ccacatgatt gtggtttcca tcacctatgg cacgtgcatt ttcatctaca tgaatcctac
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agcaaaggaa gaagtgaccg ttaataaagt agtttctttg ctcatttctt ctattttqct
                                                                     480
                                                                     486
      260
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<211>
      486
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= AF179782
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                                                                     120
gaccogtgtg gotttotgtg cocagaaggo catococcao ttotactgtg atoccagtgo
                                                                     180
tctcctqaaq ctcqcctqct cggatacccg cataaatgag ctgatgatca tcgccatggg
                                                                     240
cttgacgttc ctcactattc ccctcacact gatcgtcttc tcctacgtcc gcatctcctg
                                                                     300
ggctgtgctt ggcatctcgt ctcctggcgg gcgatgcaag gccttctcca cctgtggttc
                                                                     360
teateteacg gtggttetge tettetatgg gtetettatg ggtgtgtatt tgetteetee
                                                                     420
gtcatcttac tctacagaga gggaaagcag gctgccattc tctacatggt gatcattccc
                                                                     480
                                                                     486
atgtta
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\approx AF179783
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                                                                     120
aatgatattg cctttctgtg gcaataatgt cattgatcat attacctgtg agatcctggc
                                                                     180
                                                                     240
tettaaaete atatgeteag atattteeat gaatgtgett ateatggeag tggeaagtat
                                                                     300
tgttatattg gtgattcctc tgctgttcat ttttatctcc tatgtattca tcctctcttc
catcctgaga attaattctt ctgaggggag aaagaaagcc tttgcaacct gttcagccca
                                                                     360
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cctg	actg	tg g	tcat	ctta	t tc	tatg	gttc	ago	tctt	ttt	atgt	acat	ga a	gcct	aagtc	420
aaag	taca	ca a	aagt	atct	g at	gaaa	tcat	tgc	actg	tct	tacg	gagt	ag t	aacc	ccaat	480
gttg																484
<210 <211 <212 <213	> 4 > D	62 87 NA ulem	ur r	ubri	vent	er										
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<400 t gt Va 1	t ac	62 c at a Il	a tg .e Cy	rt ca rs Hi 5	c cc s Pr	t ct o Le	c ca u Hi	c ta s Ty	ac ac yr Th	ır Th	ec at nr Il	c at e Me	g ag et Ar	19 ga 19 Gl	a gag lu Glu	49
ctc Leu	tgc Cys	acc Thr	tta Leu 20	ttg Leu	gtg Val	gct Ala	ata Ile	tcc Ser 25	tgg Trp	ctc Leu	ctg Leu	tct Ser	tgt Cys 30	gcc Ala	agc Ser	97
tcc Ser	ctc Leu	tcc Ser 35	cac His	acc Thr	ctt Leu	ctc Leu	ctg Leu 40	acc Thr	cgg Arg	ctg Leu	tcc Ser	ttc Phe 45	tgt Cys	gct Ala	gct Ala	145
aat Asn	gtc Val 50	att Ile	ccc Pro	aac Asn	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	gct Ala	gct Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu	193
tcc Ser 65	tgc Cys	tca Ser	gac Asp	atc Ile	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttt Phe	aca Thr	gta Val	80 Gly 999	241
gtg Val	gtg Val	gtc Val	att Ile	acc Thr 85	ttg Leu	cca Pro	ttc Phe	tta Leu	tgt Cys 90	atc Ile	ctg Leu	gta Val	tct Ser	tac Tyr 95	ggc Gly	289
tac Tyr	att Ile	gly aaa	gcc Ala 100	acc Thr	atc Ile	ctg Leu	agg Arg	gtc Val 105	cct Pro	tca Ser	acc Thr	aaa Lys	ggg Gly 110	atc Ile	tgc Cys	337
aaa Lys	gca Ala	tta Leu 115	tcc Ser	acg Thr	tgt Cys	ggg ggg	tcc Ser 120	cat His	ctc Leu	tct Ser	gtg Val	gtg Val 125	tct Ser	ctg Leu	tac Tyr	385
tac Tyr	999 Gly 130	gca Ala	ata Ile	ttt Phe	Glà aaa	cag Gln 135	tac Tyr	ctt Leu	ttc Phe	cca Pro	gca Ala 140	tta Leu	agc Ser	aat Asn	tcc Ser	433
att Ile 145	gac Asp	aag Lys	gac Asp	atc Ile	att Ile 150	gtg Val	gct Ala	atg Met	atg Met	tac Tyr 155	acg Thr	gtg Val	gtc Val	aca Thr	ccc Pro 160	481
_	ttg Leu															487

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<211> 162
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Leu Cys Thr Leu Leu Val Ala Ile Ser Trp Leu Leu Ser Cys Ala Ser
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
Asn Val Ile Pro Asn Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
                        55
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
Val Val Ile Thr Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Cys
                                105
            100
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
                                                 125
        115
                            120
Tyr Gly Ala Ile Phe Gly Gln Tyr Leu Phe Pro Ala Leu Ser Asn Ser
    130
                        135
Ile Asp Lys Asp Ile Ile Val Ala Met Met Tyr Thr Val Val Thr Pro
                                         155
Met Leu
<210> 264
<211> 475
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<213> Eulemur rubriventer
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<223> Product = olfactory receptor
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 Val Ala Ile Cys Lys Pro Leu His Tyr Met Asn Ile Met Ser Arg Gln
                                       10
                                                                         97
ctg tgt cac ctt ctg gtg gct ggt tcc tgg ctg gga ggc ttt ctt cac
Leu Cys His Leu Leu Val Ala Gly Ser Trp Leu Gly Gly Phe Leu His
tct att att cag att ttt atc acc atc caa tcg ccc ttt tgt ggt ccc
                                                                         145
Ser Ile Ile Gln Ile Phe Ile Thr Ile Gln Ser Pro Phe Cys Gly Pro
aac gtg att gac cac tac ttc tgt gac ctc ctg cca tta ttc aag ctt
                                                                         193
Asn Val Ile Asp His Tyr Phe Cys Asp Leu Leu Pro Leu Phe Lys Leu
gcc tgc acc gac acc ttt gta gag ggg ctg act gtg ttg gcc aat agt
                                                                         241
Ala Cys Thr Asp Thr Phe Val Glu Gly Leu Thr Val Leu Ala Asn Ser
                                          75
                                                                         289
ggc tta att ccc gtg tgc tcc ctg ttt atc ctg gtg tcc tcc tat atc
Gly Leu Ile Pro Val Cys Ser Leu Phe Ile Leu Val Ser Ser Tyr Ile
                                                                         337
att att ctg gtg cac ttg agg aaa cat tct gca gag ggg agg cac aaa
Ile Ile Leu Val His Leu Arg Lys His Ser Ala Glu Gly Arg His Lys
             100
gcc ctc tct acc tgt gcc tct cac atc acg gtg gtc att ttg ttt ttt Ala Leu Ser Thr Cys Ala Ser His Ile Thr Val Val Ile Leu Phe Phe
                                                                         385
                             120
        115
gga cct gcc atc ttc ctc tac atg cga cct tcc tct acc ttc aca gaa
                                                                         433
Gly Pro Ala Ile Phe Leu Tyr Met Arg Pro Ser Ser Thr Phe Thr Glu
                         135
                                                                         475
gac aaa ctc atg ggt gtg ttg tac aca gtc atc acc ccc agt
Asp Lys Leu Met Gly Val Leu Tyr Thr Val Ile Thr Pro Ser
                                          155
                     150
<210> 265
<211> 158
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       PRT
<213> Eulemur rubriventer
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<221>
       misc feature
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<400> 265
Val Ala Ile Cys Lys Pro Leu His Tyr Met Asn Ile Met Ser Arg Gln
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Leu Cys His Leu Leu Val Ala Gly Ser Trp Leu Gly Gly Phe Leu His

Ser	Ile	Ile	Gln	Ile	Phe	Ile	Thr	Ile	Gln	Ser	Pro	Phe	Cys	Gly	Pro
		35					40					45			

Asn Val Ile Asp His Tyr Phe Cys Asp Leu Leu Pro Leu Phe Lys Leu 50 55 60

Ala Cys Thr Asp Thr Phe Val Glu Gly Leu Thr Val Leu Ala Asn Ser 70 75 80

Gly Leu Ile Pro Val Cys Ser Leu Phe Ile Leu Val Ser Ser Tyr Ile 85 90 95

Ile Ile Leu Val His Leu Arg Lys His Ser Ala Glu Gly Arg His Lys

Ala Leu Ser Thr Cys Ala Ser His Ile Thr Val Val Ile Leu Phe Phe 115 120 125

Gly Pro Ala Ile Phe Leu Tyr Met Arg Pro Ser Ser Thr Phe Thr Glu 130 135 140

Asp Lys Leu Met Gly Val Leu Tyr Thr Val Ile Thr Pro Ser

<210> 266

<211> 487

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc\_feature

<222> (1)..(487)

<223> Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/GenBank = AF179786

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 266

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Val Ala Ile Ser Asn Pro Pro Leu Tyr Val Gln Ala Met Pro Arg Lys
10 15

ctg tgc atc tgt ttc att atc tgt tca tac act gga ggc ttt gtt aat 97
Leu Cys Ile Cys Phe Ile Ile Cys Ser Tyr Thr Gly Gly Phe Val Asn
20 25 30

gca ata ata tta acc agc aac aca ttc acg ttg gat ttt tgt ggt gac 145
Ala Ile Ile Leu Thr Ser Asn Thr Phe Thr Leu Asp Phe Cys Gly Asp
35 40 45

aat gtc atc gac gac ttt ttc tgt gat gtc cca ccc ctg gtg aag ttg
Asn Val Ile Asp Asp Phe Phe Cys Asp Val Pro Pro Leu Val Lys Leu
50 60

gcc tgt gat gtg gaa ggg agc tac cag gct gtg ctg tac ttc ctc ctg Ala Cys Asp Val Glu Gly Ser Tyr Gln Ala Val Leu Tyr Phe Leu Leu 65 70 75 80	241
gcc tcc aac gtc atc tcc ccg gcc atg ctc atc ctc gcc tcc tac gtc Ala Ser Asn Val Ile Ser Pro Ala Met Leu Ile Leu Ala Ser Tyr Val 85 90 95	289
ttc atc atc gca gca gtc ttg agg gtc cgc tcc agc cgg ggc cgc ctc Phe Ile Ile Ala Ala Val Leu Arg Val Arg Ser Ser Arg Gly Arg Leu 100 105 110	337
aag gcc ttc tcc acg tgc tcc tcc cac ctg atc tct gtt acc tta tac Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Ser Val Thr Leu Tyr 115 120 125	385
tac ggc tcc att ctc tac atc tac tct cgc cca agt tcc agc tat tcc Tyr Gly Ser Ile Leu Tyr Ile Tyr Ser Arg Pro Ser Ser Ser Tyr Ser 130	433
ctc gag agg gac aaa atg gtc tct acc ttt tac acc gtg ctg ttc ccc Leu Glu Arg Asp Lys Met Val Ser Thr Phe Tyr Thr Val Leu Phe Pro 145 150 155 160	481
acg ctc Thr Leu	487
<210> 267 <211> 162 <212> PRT	
<213> Eulemur rubriventer  <220> <221> misc_feature	:
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<pre>&lt;213&gt; Eulemur rubriventer  &lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/GenBank = &lt;400&gt; 267  Val Ala Ile Ser Asn Pro Pro Leu Tyr Val Gln Ala Met Pro Arg Lys 1</pre>	: AF179786
<pre>&lt;213&gt; Eulemur rubriventer  &lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(487) &lt;223&gt; Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/GenBank = &lt;400&gt; 267  Val Ala Ile Ser Asn Pro Pro Leu Tyr Val Gln Ala Met Pro Arg Lys 1</pre>	AF179786
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Phe Ile Ile Ala Ala Val Leu Arg Val Arg Ser Ser Arg Gly Arg Leu 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Ser Val Thr Leu Tyr 115 120 125

Tyr Gly Ser Ile Leu Tyr Ile Tyr Ser Arg Pro Ser Ser Ser Tyr Ser 130 135 140

Leu Glu Arg Asp Lys Met Val Ser Thr Phe Tyr Thr Val Leu Phe Pro 145 150 155 160

Thr Leu

<210> 268 <211> 478 <212> DNA <213> Eulemur rubriventer <220> <221> misc\_feature (1)..(478) <222> <223> Taxon = 34829; gene = ERU163; Accession DDBJ/EMBL/GenBank = AF179787 <220> CDS <221> <222> (2)..(478) <223> Product = olfactory receptor <400> 268 t gtt gcc gta tgt aac cct ttg cat tac ctg acg gtc atg aac cgc cag 49 Val Ala Val Cys Asn Pro Leu His Tyr Leu Thr Val Met Asn Arg Gln 10 ctc tgc ctt cag ttg gtt ttt gcc tgc tgg tgt ggg ggt ttc atc cac 97 Leu Cys Leu Gln Leu Val Phe Ala Cys Trp Cys Gly Gly Phe Ile His tot gtc aca cag gtt ata ctg gtc atc cag ctg ccc ttc tgt ggc ccc 145 Ser Val Thr Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro aac aaa ttg gac agt ttc tac tgt gat gtc cca gag gtc atc aag ctg 193 Asn Lys Leu Asp Ser Phe Tyr Cys Asp Val Pro Glu Val Ile Lys Leu gcc tgc ctg gac acc tat gtg gta gaa gtg ctg atg gtt acc aac agt 241 Ala Cys Leu Asp Thr Tyr Val Val Glu Val Leu Met Val Thr Asn Ser 65 70 ggt ctg cta tct ctt gtc tgc ttc ttg gtc ttg ata ttc tct tat gcc 289 Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Ile Phe Ser Tyr Ala

337

385

acc atc ctg acc acc ctg aga act cgc ctc cac cag ggc cag agc aag

Thr Ile Leu Thr Thr Leu Arg Thr Arg Leu His Gln Gly Gln Ser Lys

gcc ttc tct acc tgt gcc tcc cac cta atg gtg gtc agc ctg atc ttt Ala Phe Ser Thr Cys Ala Ser His Leu Met Val Val Ser Leu Ile Phe

gtg Val	cca Pro 130	tgt Cys	gta Val	ttc Phe	atc Ile	tac Tyr 135	Leu	agg Arg	cct Pro	ttc Phe	tgc Cys 140	agc Ser	ttc Phe	tct Ser	gtg Val	4	33
------------	-------------------	------------	------------	------------	------------	-------------------	-----	------------	------------	------------	-------------------	------------	------------	------------	------------	---	----

gat aag ata ttc tct gtg ttt tac atg gtg atc aca cct atg ttg Asp Lys Ile Phe Ser Val Phe Tyr Met Val Ile Thr Pro Met Leu 478 155 150

<210> 269 <211> 159

<212> PRT

<213> Eulemur rubriventer

<220>

<221> misc\_feature

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<223> Taxon = 34829; gene = ERU163; Accession DDBJ/EMBL/GenBank = AF179787

<400> 269

Val Ala Val Cys Asn Pro Leu His Tyr Leu Thr Val Met Asn Arg Gln

Leu Cys Leu Gln Leu Val Phe Ala Cys Trp Cys Gly Gly Phe Ile His

Ser Val Thr Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro

Asn Lys Leu Asp Ser Phe Tyr Cys Asp Val Pro Glu Val Ile Lys Leu 50

Ala Cys Leu Asp Thr Tyr Val Val Glu Val Leu Met Val Thr Asn Ser

Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Ile Phe Ser Tyr Ala

Thr Ile Leu Thr Thr Leu Arg Thr Arg Leu His Gln Gly Gln Ser Lys 105

Ala Phe Ser Thr Cys Ala Ser His Leu Met Val Val Ser Leu Ile Phe 120

Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val 130

Asp Lys Ile Phe Ser Val Phe Tyr Met Val Ile Thr Pro Met Leu 155

<210> 270

<211> 487

<212> DNA

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<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 34829; gene = ERU164; Accession DDBJ/EMBL/GenBank = AF179788
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<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
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                                                                       49
  Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Ile Ser Thr Arg
                                      10
                                                                       97
gtt tgt atc ctt ctt gtc tgt agc tcc tgg ctt gca gga ttc ttg atc
Val Cys Ile Leu Leu Val Cys Ser Ser Trp Leu Ala Gly Phe Leu Ile
                                25
atc ttt cca cca ata atc ctt ctt ctg cag ttg gac ttc tgt gcc tcc
                                                                      145
Ile Phe Pro Pro Ile Ile Leu Leu Leu Gln Leu Asp Phe Cys Ala Ser
                                                                      193
aat ata att gat cat ttt atc tgt gat tct tct cca att ctg cag ctt
Asn Ile Ile Asp His Phe Ile Cys Asp Ser Ser Pro Ile Leu Gln Leu
                        55
    50
tet tgt aca aac act cac ttt cta gaa ctc atg gca ttt tgt tta gcc
                                                                      241
Ser Cys Thr Asn Thr His Phe Leu Glu Leu Met Ala Phe Cys Leu Ala
gtg gtg aca ctc atg gtc acc ttg acc tta gtt att ctc tcc tat aca
                                                                      289
Val Val Thr Leu Met Val Thr Leu Thr Leu Val Ile Leu Ser Tyr Thr
                                    90
aat att atc cgg aca att cta aga att cct tct atg agt caa agg aaa
                                                                      337
Asn Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Met Ser Gln Arg Lys
            100
aaa gcc ttt tcc act tgt tcc tcc cat ata ata gtt gtt tcc ctc tct
                                                                      385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Ser
                            120
        115
tat ggt agt tgt atc ttc atg tac ata aag cct tct aca agg gaa agg
                                                                      433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Thr Arg Glu Arg
                        135
gtg act tta agc aaa gga gta gct gtg gtt aat act tca gtg gct cct
                                                                      481
Val Thr Leu Ser Lys Gly Val Ala Val Val Asn Thr Ser Val Ala Pro
                     150
                                         155
145
                                                                       487
ctt ttg
Leu Leu
 <210> 271
 <211> 162
 <212> PRT
 <213> Eulemur rubriventer
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 <222> (1)..(487)
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<223> Taxon = 34829; qene = ERU164; Accession DDBJ/EMBL/GenBank = AF179788 <400> 271

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Ile Phe Pro Pro Ile Ile Leu Leu Leu Gln Leu Asp Phe Cys Ala Ser

Asn Ile Ile Asp His Phe Ile Cys Asp Ser Ser Pro Ile Leu Gln Leu

Ser Cys Thr Asn Thr His Phe Leu Glu Leu Met Ala Phe Cys Leu Ala 70

Val Val Thr Leu Met Val Thr Leu Thr Leu Val Ile Leu Ser Tyr Thr 85

Asn Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Met Ser Gln Arg Lys 105

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Ser 120

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Thr Arg Glu Arg

Val Thr Leu Ser Lys Gly Val Ala Val Val Asn Thr Ser Val Ala Pro 160 150

Leu Leu

<210> 272

<211> 483

<212> DNA <213> Eulemur rubriventer

<220>

<221> misc\_feature

(1)..(483) <222>

<223> Taxon = 34829; gene = ERU165; pseudogene; Accession DDBJ/EMBL/GenBank = AF179789

<400> 272

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ageteatect egectgetgg etggeagggt teteetteat cattgtgeet gteateetga 120

ccagtcagct tccattctgt gacacccaca tcaaccactt cttctgtgac tatacacctc 180

taat	ggag	gt gg	grer	gcag	999	Jeca	aayy	tge	Lyga	yac	9919	gatti	L a		ggccc	240
tggt	ggca	ct g	ctca	gcac	c tt	ggtg	ctga	tca	ccct	gtc	ctac	atcca	ag a	tcat	cagga	300
cgati	tgtc	ag ga	atcc	cctct	gt	ccag	gaga	gga	aaaa	ggc	tttc	tccad	cc t	gttc	ctccc	360
atgt	catc	gt g	gtta	ccat	g tg	ctate	ggaa	gct	gttt	ttt	tatg	tatgi	tc a	agcc	ctccc	420
cagg	caaa	gg g	gttg	atcta	a aa	caaa	ggag	tgt	ctta	atc	aata	caati	ta t	tgcc	cccct	480
ctt																483
<210 <211 <212 <213 <220	> 4 > D > E			ubri	vent	er										
<221 <222 <223	> (	isc_ 1) axon	(486	)	; ge	ne =	ERU	167;	Acc	essi	on D	DBJ/	EMBL	/Gen	Bank =	- AF179790
<220 <221 <222 <223	> C > (	DS 2) rodu		) olf	acto	ry r	ecep	tor								
<400 t gt Va 1	a ac	73 c at a Il	c tg e Cy	t ca s Hi 5	c cc s Pr	t ct o Le	g ag u Ar	a ta g Ty	ic ac vr Th	r As	ac at sp Il	c at e Me	g ac t Th	t co ir Pr 15	t cgt o Arg	49
ctg Leu	tgt Cys	ggt Gly	ctg Leu 20	ctg Leu	gtt Val	tca Ser	ctt Leu	tcc Ser 25	ctg Leu	tcc Ser	att Ile	tgc Cys	tcc Ser 30	gcg Ala	gat Asp	97
gcc Ala	ctg Leu	ctc Leu 35	cac His	agc Ser	ctc Leu	atg Met	ctg Leu 40	ctg Leu	cag Gln	ctg Leu	tcc Ser	ttc Phe 45	tgc Cys	aca Thr	gac Asp	145
ctt Leu	gaa Glu 50	atc Ile	tcc Ser	ctt Leu	ttc Phe	ttc Phe 55	tgt Cys	gaa Glu	gtc Val	gtt Val	cag Gln 60	gtc Val	gtc Val	aag Lys	ctc Leu	193
gcg Ala 65	tgc Cys	tcc Ser	gat Asp	acc Thr	ctc Leu 70	gtc Val	aac Asn	aac Asn	ctt Leu	ctg Leu 75	atc Ile	tat Tyr	ttt Phe	gca Ala	gct Ala 80	241
tgc Cys	acc Thr	ttg Leu	ggt Gly	ggc Gly 85	att Ile	cct Pro	ctg Leu	tct Ser	ggc Gly 90	atc Ile	att Ile	ttt Phe	tct Ser	tac Tyr 95	act Thr	289
caa Gln	ata Ile	gcc Ala	acc Thr 100	tcc Ser	att Ile	ttg Leu	aaa Lys	atg Met 105	ccg Pro	tca Ser	tcg Ser	ggc Gly	aga Arg 110	aag Lys	tat Tyr	337
aaa Lys	gcc Ala	ttt Phe 115	tcc Ser	acc Thr	tgt Cys	Gly aaa	tct Ser 120	cac His	ctg Leu	tca Ser	gtt Val	gtt Val 125	tcc Ser	ctg Leu	ttc Phe	385
tat Tyr	999 Gly 130	Thr	ggt Gly	ttg Leu	ggg Gly	gtg Val 135	tac Tyr	atc Ile	agt Ser	tct Ser	gca Ala 140	gtt Val	tct Ser	gac Asp	tct Ser	433
t.ca	agg	agg	act	aca	ata	gct	tca	gtg	atg	tac	act	gtg	gtc	act	ccc	481

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Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
                    150
                                         155
                                                                        486
tgt tg
Cys
<210> 274
<211> 161
<212> PRT
<213> Eulemur rubriventer
<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 34829; gene = ERU167; Accession DDBJ/EMBL/GenBank = AF179790
<400> 274
Val Ala Ile Cys His Pro Leu Arg Tyr Thr Asp Ile Met Thr Pro Arg
Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp
             20
Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp
                             40
Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu
Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala
Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr
                 85
                                      90
Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr
             1.00
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser
     130
 Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
                                          155
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Cys

<210> 275 <211> 487

<212> DNA <213> Eulemur rubriventer	
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ctg tgt ggt ctg ctg gtt tca ctt tcc ctg tcc att tgc tcc gcg gat Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp 20 25 30	97
gcc ctg ctc cac agc ctc atg ctg ctg cag ctg tcc ttc tgc aca gac Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp 35 40 45	145
ctt gaa atc tcc ctt ttc ttc tgt gaa gtc gtt cag gtc gtc aag ctc Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu 50 55 60	193
gcg tgc tcc gat acc ctc gtc aac aac ctt ctg atc tat ttt gca gct Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala 65 70 75 80	241
tgc acc ttg ggt ggc att cct ctg tct ggc atc att ttt tct tac act Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr 85 90 95	289
caa ata gcc acc tcc att ttg aaa atg ccg tca tcg ggc aga aag tat Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr 100 105 110	337
aaa gcc ttt tcc gcc tgt ggg tct cac ctg tca gtt gtt tcc ctg ttc Lys Ala Phe Ser Ala Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125	385
tat ggg aca ggt ttg ggg gtg tac atc agt tct gca gtt tct gac tct Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser 130 135 140	433
tca agg agg act gcg gtg gct tca gtg atg tac act gtg gtc act ccc Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155 160	481
gtg ttg Val Leu	487
<210> 276 <211> 162 <212> PRT <213> Eulemur rubriventer	
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Val Ala Ile Cys His Pro Leu Thr Tyr Thr Asp Ile Met Thr Pro Arg 1.0

Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp

Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp

Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu 50 55

Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala

Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr

Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr 100

Lys Ala Phe Ser Ala Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120 115

Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser 135 130

Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 155 150

Val Leu

<210> 277 <211> 486

<212> DNA <213> Macaca sylvanus

<220>

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(1)..(486)

<223> Taxon = 9546; gene = MSY172; Accession DDBJ/EMBL/GenBank = AF179792

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(1)..(486) <222>

<223> Product = olfactory receptor

<400> 277

cct gcc atc tgc cag cca ctc agg tac cgc gtg ctc atg aac cac cgg

48

Pro Al	la	Ile	Cys	Gln 5	Pro	Leu	Arg	Tyr	Arg 10	Val	Leu	Met	Asn	His 15	Arg		
ctc to	gt ys	gtg Val	ctg Leu 20	ctg Leu	gtg Val	gga Gly	gct Ala	gcc Ala 25	tgg Trp	gtc Val	ctc Leu	tgc Cys	ctc Leu 30	ctc Leu	aag Lys		96
tog gt Ser Va	al	act Thr 35	gag Glu	aca Thr	gtc Val	att Ile	gcc Ala 40	atg Met	agg Arg	ctg Leu	ccc Pro	ttc Phe 45	tgt Cys	ggc Gly	cac His		144
cac go His Va	al	gtc Val	agt Ser	cac His	ttc Phe	acc Thr 55	tgc Cys	gag Glu	atc Ile	ctg Leu	gcg Ala 60	gtg Val	ctg Leu	aag Lys	ctg Leu		192
acg to Thr C	gc 'ys	ggt Gly	aac Asn	aca Thr	tcg Ser 70	gtc Val	agc Ser	gag Glu	gtc Val	ttc Phe 75	ctg Leu	ctg Leu	gtg Val	ggc Gly	tcc Ser 80		240
atc c	tg .eu	ctg Leu	ctg Leu	cct Pro 85	gtg Val	ccc Pro	ctg Leu	gca Ala	ttc Phe 90	att Ile	tgc Cys	ctg Leu	tcc Ser	tac Tyr 95	ttg Leu		288
ctc a Leu I	tc le	ctg Leu	gcc Ala 100	acc Thr	atc Ile	ctg Leu	agg Arg	gtg Val 105	ccc Pro	tca Ser	gct Ala	gct Ala	999 Gly 110	tgc Cys	cgc Arg		336
aaa g Lys A	gcc Ala	ttc Phe 115	tcc Ser	acc Thr	tgc Cys	tca Ser	gca Ala 120	cac His	ctg Leu	gct Ala	gtg Val	gtg Val 125	ctg Leu	ctt Leu	ttc Phe		384
tac a Tyr S	agc Ser L30	acc Thr	atc Ile	atc Ile	ttc Phe	acg Thr 135	tac Tyr	atg Met	aag Lys	ccc Pro	aag Lys 140	agc Ser	aag Lys	gaa Glu	gcc Ala		432
cac a His I 145	atc [le	tct Ser	gat Asp	gag Glu	gtc Val 150	Phe	aca Thr	gtc Val	ctc Leu	tac Tyr 155	gcc Ala	atg Met	gtc Val	aca Thr	ccc Pro 160		480
atg t Met L	_																486
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<400>	> 2	278												*			
Pro <i>P</i>	Ala	Ile	Cys	Glr 5	Pro	Leu	Arg	ј Туг	Arg 10	y Val	. Leu	. Met	. Asn	His 15	Arg		
Leu (	Cys	Val	Leu 20	. Lev	ı Val	. Gly	Ala	Ala 25	a Trp	val	. Lev	ı Cys	30	ı Lev	Lys		
Ser \	Val	Thr 35	Glu	ı Thi	val	l Ile	Ala 40	a Met	: Arg	g Leu	ı Pro	Phe 45	е Суя	s Gly	, His		

His Val Val Ser His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu

Thr Cys Gly Asn Thr Ser Val Ser Glu Val Phe Leu Leu Val Gly Ser

Ile Leu Leu Pro Val Pro Leu Ala Phe Ile Cys Leu Ser Tyr Leu

Leu Ile Leu Ala Thr Ile Leu Arg Val Pro Ser Ala Ala Gly Cys Arg 100 105

Lys Ala Phe Ser Thr Cys Ser Ala His Leu Ala Val Val Leu Leu Phe 120

Tyr Ser Thr Ile Ile Phe Thr Tyr Met Lys Pro Lys Ser Lys Glu Ala 140

His Ile Ser Asp Glu Val Phe Thr Val Leu Tyr Ala Met Val Thr Pro 150

Met Leu

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<212> DNA

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(1)..(489) <222>

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<210> 280

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<213> Macaca sylvanus
<220>
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       Taxon = 9546; gene = MSY174; Accession DDBJ/EMBL/GenBank = AF179794
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      CDS
<222>
       (2)..(481)
<223> product = olfactory receptor
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                                                                          49
  Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro
                                       10
atg tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat
Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
                                                                          97
            20
gga ggg atc cag act ttg ttc ata gcc cac tta cca ttc tgt ggc cct
                                                                         145
Gly Gly Ile Gln Thr Leu Phe Ile Ala His Leu Pro Phe Cys Gly Pro
        35
aat gtc atc gac cac ttt atg tgt gat tta gta cct ctt cta gag ctg
                                                                         193
Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
                         55
gee tge aca gae act cae ace ttg ggg eet etg ata get gee aac agt
                                                                         241
Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
                                                                         289
gga tca ttg tgt ttc ctc att ttt tcc atg ctg gtt gct tcc tat gtc
Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
                                      90
                 85
                                                                         337
atc atc ctg tgc tcc cta agg act cat atc tct gaa ggg cgt cac aaa
Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
                                                       110
             100
gtt ctg tct agt tgt acc tct cat atc ttt gtt gtc atc tta ttc ttt
                                                                         385
Val Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
                                                   125
                              120
gtc cct tgt tca tac ctg tat cta aga cct cta acc tcc ttc ttc ccc
                                                                         433
Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Phe Pro
     130
act gac aaa gct gtg act gtg ttt tgc acc cta ttt aca cct atg ttg
                                                                         481
Thr Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
145
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        281
       160
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        PRT
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<223> Taxon = 9546; gene = MSY174; Accession DDBJ/EMBL/GenBank = AF179794
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Val	Ala	Ile	Cys	Lys	Pro	Leu	His	Tyr	Ala	Thr	Ile	Met	Ser	Gln	Pro
1			-	5				_	10					15	

Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His 20

Gly Gly Ile Gln Thr Leu Phe Ile Ala His Leu Pro Phe Cys Gly Pro

Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu

Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser

Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val 95

Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys 100

Val Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe 115

Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Phe Pro 130

Thr Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu 150 155

282 <210>

<400> 281

402 <211>

<212> DNA

<213> Macaca sylvanus

<220>

misc\_feature <221>

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Taxon = 9546; gene = MSY175; pseudogene; Accession DDBJ/EMBL/GenBank <223> = AF179795\*

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<210> 283
<211> 487
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      DNA
<213> Macaca sylvanus
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       Taxon = 9546; gene = MSY176; Accession DDBJ/EMBL/GenBank = AF179796
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       CDS
<222>
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<223> Product = olfactory receptor
<400> 283
c gtg gct att tgc aac cct ctg ctc tac gca tta gtg gtg tct cca aag
                                                                             49
  Val Ala Ile Cys Asn Pro Leu Leu Tyr Ala Leu Val Val Ser Pro Lys
gta tgt cgt ctg ctg gtg tcc ctc aca tac ctt cag agt ctt atc aca
                                                                             97
Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile Thr
gcc ctt act gtc tct tcc tgt gtg ttc tct gtg tca tac tgt tct tcc
Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser Ser
                                                                            145
         35
                                                                            193
aac atc atc aac cat ttt tac tgt gac gat gtc cct ttg cta gca ttg
Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Ala Leu
                           55
teg tgt tet gat ace tae att cea gaa aca gea gtg ttt ate ttt tea
                                                                            241
Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe Ser
65
                                                                             289
ggg acc aat ttg ttt ttc tcc atg acc gtt gtt ctg ata tcc tac ttc
Gly Thr Asn Leu Phe Phe Ser Met Thr Val Val Leu Ile Ser Tyr Phe
                                        90
aac att gtt att acc att ttg agg ata cgt tcc tca gaa gga cga caa
                                                                             337
Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Gln
                                    105
aaa gcc ttt tcc acg tgt gct tct cac atg ata gct gtg gtt gtg ttc
Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Phe
                                                                             385
                                                                             433
 tat ggg act ctc ctt ttc atg tat ttg caa cca agg agt aat cac tca
 Tyr Gly Thr Leu Leu Phe Met Tyr Leu Gln Pro Arg Ser Asn His Ser
 tta gat act gac aaa atg gcc tcg gtc ttc tac acc ctg atc ata cct
                                                                             481
 Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Ile Ile Pro
                                                                   160
                       150
 145
                                                                             487
 atg ttg
 Met Leu
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<220>

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<211> 162
<212> PRT
<213> Macaca sylvanus
<220>
<221> misc_feature
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Val Ala Ile Cys Asn Pro Leu Leu Tyr Ala Leu Val Val Ser Pro Lys
Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile Thr
             20
Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser Ser
                              40
Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala Leu
Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe Ser
Gly Thr Asn Leu Phe Phe Ser Met Thr Val Val Leu Ile Ser Tyr Phe
                                                            95
Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Gln
Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Phe
         115
Tyr Gly Thr Leu Leu Phe Met Tyr Leu Gln Pro Arg Ser Asn His Ser
     130
 Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Ile Ile Pro
                      150
 Met Leu
 <210> 285
 <211> 487
<212> DNA
 <213> Macaca sylvanus
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 <223> Taxon = 9546; gene = MSY177; Accession DDBJ/EMBL/GenBank = AF179797
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<221> CDS
<222>
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<223> Product = olfactory receptor
<400> 285
t gtg gcc atc tgt cac cct cta cat tat gcc atc atc atg ggt cag agt
                                                                          49
  Val Ala Ile Cys His Pro Leu His Tyr Ala Ile Ile Met Gly Gln Ser
cag tgt gtc acg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt
                                                                          97
Gln Cys Val Thr Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
            20
gct ctt ttg cac act ctc ctc ctg gcc tgg ctt tcc ttc tgt gct gat
                                                                         145
Ala Leu Leu His Thr Leu Leu Leu Ala Trp Leu Ser Phe Cys Ala Asp
                                                                         193
cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
                         55
                                              60
tee tge tea gae ace tee etc aat eag tta gea ate ttt aca gea gga
                                                                         241
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
ttg aca gcc att atg ctt cca ttc ctg tgt atc ctg gtt tct tat ggt
                                                                         289
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                                      90
                 85
                                                                         337
cac act gca gtc acc atc ctc cag att ccc tct act aat ggc ata tgc
His Thr Ala Val Thr Ile Leu Gln Ile Pro Ser Thr Asn Gly Ile Cys
                                  105
             100
aaa gcc ttg tcc act tgt gga tcc cac ctc tca gca gtg act ctc tat
                                                                         385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Ala Val Thr Leu Tyr
                                                   125
tat ggg acc att att ggt ctc tat ttt ctt ccc cca tcc agc aac act
                                                                         433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
                         135
    130
aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                                                                         481
                     150
                                                                         487
atg ttg
Met Leu
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       162
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Val Ala Ile Cys His Pro Leu His Tyr Ala Ile Ile Met Gly Gln Ser
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Gln Cys Val Thr Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
                                  25
            20
Ala Leu Leu His Thr Leu Leu Leu Ala Trp Leu Ser Phe Cys Ala Asp
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
                                       90
His Thr Ala Val Thr Ile Leu Gln Ile Pro Ser Thr Asn Gly Ile Cys
                                  105
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Ala Val Thr Leu Tyr
                              120
         115
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
                          135
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                                           155
                      150
Met Leu
<210> 287
<211> 487
<212> DNA
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<223> product = olfactory receptor
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                                                                            49
  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gta ctg acc acc ttc cat
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                                                                            97
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25

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp

35 40 aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg 193 Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 55 gcc tgc tct gac act caa gtt aat gaa ttg gcg ata ttt atc acg gga 241 Ala Cys Ser Asp Thr Gln Val Asn Glu Leu Ala Ile Phe Ile Thr Gly 75 70 ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 289 90 cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag ggt atc tgc Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 337 100 385 aag goo tto tot act tgt ggo too cac ctc tot gtg gtg toa ctg tto Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120 433 tat ggg acc gtt att ggt ctc tac ttc tgc cca tca gct aat agt tct Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser 135 act cta aag gag act gtc atg gct atg atg tac act gtg gtg acc ccc Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 481 155 487 atg ctg Met Leu <210> 288

<211> 162

<212> PRT

<213> Macaca sylvanus

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Taxon = 9546; gene = MSY178; Accession DDBJ/EMBL/GenBank = AF179798

<400> 288

Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met 10

Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 20

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 40 35

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 55

Ala Cys Ser Asp Thr Gln Val Asn Glu Leu Ala Ile Phe Ile Thr Gly 75

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Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
                                105
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
                                        155
Met Leu
<210> 289
<211>
       484
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       DNA
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<223> Taxon = 9546; gene = MSY179; Accession DDBJ/EMBL/GenBank = AF179799
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<222> (2)..(484)
<223> Product = olfactory receptor
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                                                                       49
  Cys Ala Ile Cys Cys Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys
                                                                       97
 ctc tgt atc tta ctc ctt tcc ttg tgt tgg gtc tta tct gtg ctc tat
Leu Cys Ile Leu Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr
                                 25
             20
 ggc ctc ata cac acc ttc ctc atg acc acg gtg acc ttc tgt ggg tca
                                                                      145
 Gly Leu Ile His Thr Phe Leu Met Thr Thr Val Thr Phe Cys Gly Ser
 cga aaa atc cac tac atc ttc tgt gag atg tat gta ttg ctg agg ctg
                                                                       193
 Arg Lys Ile His Tyr Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Leu
                                             60
 gca tgt tcc gac act cag att aat cac aca gtg ctg att gcc aca ggc
                                                                       241
 Ala Cys Ser Asp Thr Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly
                     70
 tgc ttt atc ttc ctc att ccc ttt gga ttc atg atc att tcc tat gtg
                                                                       289
 Cys Phe Ile Phe Leu Ile Pro Phe Gly Phe Met Ile Ile Ser Tyr Val
                                     90
                 85
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ttg att gtc aga gcc atc ctc aga ata ccc tca gtc tct aag aaa tac

Leu I	le Va	l Arg 100	Ala	Ile	Leu	Arg	Ile 105	Pro	Ser	Val	Ser	Lys 110	Lys	Tyr		
aaa g Lys A	cc tt la Ph	e Ser	act Thr	tgt Cys	gcc Ala	tcc Ser 120	cat His	ttg Leu	ggt Gly	gta Val	gtc Val 125	tcc Ser	ctc Leu	ttc Phe		385
tat g Tyr G 1	gg ac ly Th	a ctt r Leu	tgt Cys	atg Met	gta Val 135	tac Tyr	ctg Leu	aag Lys	ccc Pro	ctc Leu 140	cat His	acc Thr	tac Tyr	tct Ser		433
gtg a Val L 145	ag ga ys As	c tca p Ser	gta Val	gcc Ala 150	aca Thr	gtg Val	atg Met	tat Tyr	gcg Ala 155	gtg Val	gtg Val	aca Thr	ccc Pro	atg Met 160		481
atg Met							•									484
<210><211><211><212><213>	161 PRT	=	ylva	nus												
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Leu (	Cys I	le Lei 20	ı Leu	Leu	Ser	Leu	Cys 25	Trp	Val	Leu	Ser	Val 30	Leu	Tyr		
Gly I	Leu II	le His	s Thr	Phe	Leu	Met 40	Thr	Thr	Val	Thr	Phe 45	Cys	Gly	Ser		
	Lys I 50	le Hi	s Tyr	· Ile	Phe 55	Сув	Glu	. Met	Tyr	Val 60	Leu	. Leu	Arg	Leu		
Ala (	Cys S	er As	o Thr	Gln 70	Ile	: Asn	His	s Thr	Val	Leu	Ile	. Ala	Thr	Gly 80		
Cys :	Phe I	le Ph	e Leu 85	ı Ile	Pro	Phe	Gly	Phe	. Met	Ile	: Ile	e Ser	Tyr 95	· Val		
Leu	Ile V	al Ar 10		a Ile	e Leu	ı Arg	11e		Ser	· Val	. Sei	Lys 110	Lys	. Tyr		
Lys .		he Se 15	r Thi	c Cys	s Ala	Ser 120		ș Lev	ı Gly	v Val	. Val	l Ser	Lev	ı Phe		
Tyr	Gly T 130	hr Le	u Cys	s Met	Va]		Le	ı Lys	s Pro	Leu 140	ı His	s Thi	ту1	s Ser		

Met

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                                                                     120
gacccagctg tctttctgtg ctgcgaacac catcccccac atcttctgtg accttgctgc
                                                                     180
cctgctcaag ctgtcctggt cagatatctt cctcaatgag ctggtcatgt tcacagtagg
                                                                     240
ggtggtggtc attaccctgc cattcatgtg tatcctggta tcatatggct acactggggc
                                                                     300
caccatcctg agggtccctt caaccaaagg gatccacaaa gcattgtcca catgtgcctc
                                                                     360
ccatctctct gtggtttctc tctattatgg gtcaatattt ggccagtaac atttcccaac
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gacccagctg tetttetgtg etgegaacae cateccecae atettetgtg acettgetge
                                                                      180
cctgctcaag ctgtcctggt cagatatctc cctcaatgag ctggtcatgt tcacagtagg
                                                                      240
ggtggtggtc attaccctgc cattcatgtg tatcctggta tcatatggct acactggggc
                                                                      300
caccatcctg agggtccctt caaccaaagg gatccacaaa gcattgtcca catgtgcctc
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ccatctctct gtggtttctc tctattatgg gtcaatattt ggccagtaac atttcccaac
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250

Val Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr Pro Met

155

tgtaa	gcag	gt t	ctatt	gac	a ag	gatg	ttac	tgt	ggct	ctc .	atgt	acato	cg t	ggtc	acacc	480
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att Ile	Val	cca Pro 35	cca Pro	ctg Leu	agc Ser	tta Leu	ggc Gly 40	ctc Leu	cag Gln	ctc Leu	gaa Glu	ttc Phe 45	tgt Cys	ggc Gly	tcc Ser	145
aat Asn	gcc Ala 50	att Ile	gat Asp	cat His	ttt Phe	agc Ser 55	tgt Cys	gat Asp	gca Ala	ggt Gly	cct Pro 60	ctc Leu	cta Leu	aag Lys	atc Ile	193
tca Ser 65	tgc Cys	tca Ser	gac Asp	aca Thr	tgg Trp 70	gta Val	ata Ile	gaa Glu	cag Gln	ata Ile 75	gtt Val	ata Ile	ctt Leu	atg Met	gct Ala 80	241
gta Val	ttt Phe	gca Ala	ctc Leu	att Ile 85	atc Ile	acc Thr	cta Leu	gtt Val	tgt Cys 90	gtg Val	att Ile	ctg Leu	tcc Ser	tac Tyr 95	ttg Leu	289
tac Tyr	ata Ile	gtc Val	aga Arg 100	aca Thr	att Ile	ctg Leu	Arg	ttc Phe 105	cct Pro	Ser	gtt Val	GIN	GIII	Arg	aaa Lys	337
aag Lys	gcc Ala	ttt Phe 115	tct Ser	acc Thr	tgt Cys	tca Ser	tcc Ser 120	His	atg Met	att Ile	gtg Val	gtt Val 125	tcc Ser	att Ile	gcc Ala	385
tat Tyr	gga Gly 130	agc Ser	tgc Cys	atc Ile	ttc Phe	gtc Val 135	Tyr	atc Ile	aag Lys	ccc Pro	tct Ser 140	gca Ala	aaa Lys	gat Asp	gaa Glu	433
gtg Val 145	gcc Ala	ata Ile	aat Asn	aaa Lys	gga Gly 150	Val	tca Ser	gtt Val	ctt Leu	act Thr 155	Thr	tct Ser	gtt Val	gca Ala	ccc Pro 160	481
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Val Cys Thr Leu Leu Val Leu Cys Ser Trp Val Ala Gly Leu Met Ile
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Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Gly Ser
Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Ile Val Ile Leu Met Ala
Val Phe Ala Leu Ile Ile Thr Leu Val Cys Val Ile Leu Ser Tyr Leu
Tyr Ile Val Arg Thr Ile Leu Arg Phe Pro Ser Val Gln Gln Arg Lys
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
                            120
Tyr Gly Ser Cys Ile Phe Val Tyr Ile Lys Pro Ser Ala Lys Asp Glu
Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
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                    150
Leu Leu
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 Val Ala Ile Cys Arg Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
gtc tgt gcc cta atc ctt gca ttg tgc tgg gtc ctc acc aat gtt gtt
                                                                          97
Val Cys Ala Leu Ile Leu Ala Leu Cys Trp Val Leu Thr Asn Val Val
                                                                         145
gcc ctg act cac aca ctc ctc atg gct cga ctg tcc ttc tgt gtg act
Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
                                                                         193
ggg gaa ata gct cac ttt ttc tgt gac atc act cct gtc ctg aag cta
Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
tca tgt tct gac acc cac atc aac gag atg atg gtt ttt gtc ttg gga
Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
                                                                         241
                     70
ggc aca gta ctc att gtc ccc ttt ata tgc att gtc acc tcc tac atc
                                                                         289
Gly Thr Val Leu Ile Val Pro Phe Ile Cys Ile Val Thr Ser Tyr Ile
                                                                         337
cac att gtg cct gct atc ctg agg gtc cga acc tgt ggt ggg gcg ggc
His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Cys Gly Gly Ala Gly
                                  105
                                                                         385
aag gcc ttt tcc acc tgc agt tcc cac ctc tgc att gtt tgt ata ttc
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Ile Phe
                             120
                                                  125
                                                                         433
tat ggg acc ctc ttc agt gcc tac ctg tgt cct ccc tct att gcc tct
Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
gaa gag aag gac att gca gca gct gca ctg tat acc ata gtg act ccc
                                                                         481
Glu Glu Lys Asp Ile Ala Ala Ala Ala Leu Tyr Thr Ile Val Thr Pro
                     150
                                                                         487
atg ttg
Met Leu
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Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr

Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu

Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly 75

Gly Thr Val Leu Ile Val Pro Phe Ile Cys Ile Val Thr Ser Tyr Ile

His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Cys Gly Gly Ala Gly

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Ile Phe 120 115

Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser 130

Glu Glu Lys Asp Ile Ala Ala Ala Ala Leu Tyr Thr Ile Val Thr Pro 150

Met Leu

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ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn 3.0 20

48

tcc tca Ser Ser	tta ( Leu ( 35	caa Gln	acc Thr	tta Leu	ata Ile	gtg Val 40	ctg Leu	cgg Arg	ctt Leu	tcc Ser	ttc Phe 45	tgc Cys	aca Thr	gac Asp	144
ttg gaa Leu Glu 50	atc (	ccc Pro	cgc Arg	ttt Phe	ttc Phe 55	tgc Cys	gaa Glu	ctt Leu	aat Asn	cag Gln 60	gtc Val	atc Ile	cac His	ctt Leu	192
gcc tgt Ala Cys 65	tct (	gac Asp	act Thr	ttt Phe 70	ctt Leu	aat Asn	gat Asp	gtg Val	gtg Val 75	atg Met	tat Tyr	ttg Leu	gcc Ala	gct Ala 80	240
gtg ctg Val Leu	ctg Leu	Gly aaa	ggt Gly 85	ggt Gly	ccc Pro	ctt Leu	gca Ala	90 999	att Ile	ctt Leu	tac Tyr	tct Ser	tac Tyr 95	tct Ser	288
aag ata Lys Ile	Val	tcc Ser 100	tcc Ser	ata Ile	cgt Arg	gca Ala	atc Ile 105	tca Ser	tca Ser	gct Ala	cag Gln	999 Gly 110	aag Lys	tac Tyr	336
aag gca Lys Ala	ttt Phe 115	tcc Ser	acc Thr	tgt Cys	gta Val	tct Ser 120	cac His	atc Ile	tta Leu	att Ile	gtc Val 125	tcc Ser	tta Leu	ttt Phe	384
tat ggt Tyr Gly 130	Thr	ctc Leu	cta Leu	ggt Gly	gtg Val 135	tac Tyr	ctt Leu	agt Ser	tct Ser	gct Ala 140	gca Ala	act Thr	ggc Gly	aac Asn	432
tca cat Ser His 145	tca Ser	aga Arg	gct Ala	gca Ala 150	gcc Ala	tcg Ser	gtg Val	atg Met	tac Tyr 155	act Thr	gtg Val	gtc Val	acc Thr	ccc Pro 160	480
atg ctg Met Leu															486
<210><211><211><212><213>	298 162 PRT Call:	ithr	ix j	acch	us										
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Val Ala 1	a Ile	Cys	His 5	Pro	Leu	. His	з Туг	Thr 10	Val	Thr	: Ile	e Asr	Pro 15	Arg	
Leu Cys	s Gly	Leu 20	Leu	ı Val	Leu	ı Ala	a Sei 25	c Trp	o Ile	e Lei	ı Ser	30	ı Leı	ı Asn	
Ser Se	r Leu 35	Gln	Thi	: Lev	ı Ile	e Val 40	l Lei	ı Arç	g Lei	ı Sei	c Phe 45	е Суя	s Thi	Asp	
Leu Gl 50		Pro	Arç	g Phe	e Phe 55	e Cys	s Gl	u Lei	ı Ası	n Gli 60	n Val	l Ile	e Hi	s Leu	
Ala Cy	s Ser	Asp	Th:	r Phe	e Lei	ı Ası	n As	p Vai		l Me	t Ty:	r Le	u Ala	a Ala	

Val Leu Cly Cly Cly Pro Leu Ala Cly Ile Leu Tyr Ser Tyr Ser 85 90 95

70

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gl<br/>n Gly Lys Tyr 100 105 110

Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe 115 120 125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 130 135 140

Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

<210> 299 <211> 487 <212> DNA <213> Callithrix jacchus <220> misc\_feature <221> <222> (1)...(487)Taxon = 9483; gene = CJA171; Accession DDBJ/EMBL/GenBank = AF179805 <223> <220> <221> CDS (2)..(487) <222> <223> Product = olfactory receptor <400> 299 c gtg gcc atc tgt aac cca ctg ttg tac atg gtc acc atg tct ccc cag 49 Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln 5 gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gct ttg ggg 97 Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ala Leu Gly gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt gca gaa 145 Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ala Glu acc ctt gtc aat cac tac atg tgt gac atc ctt ccc ctc ctt gag ctc 193 Thr Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu 55 50 241 tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Phe Ile Ile Val 70 acc att ggc att ggg gtg ccc att gtc acc att ttt atc tct tat ggt Thr Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 289 90 85

ttt att ctt tcc agc att ctc cac att agt tct gct gag ggc agg tct  Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Ala Glu Gly Arg Ser  100 105 110	,
aaa gcc ttc agt acc tgc agc tcc cac ata gtt gtg gta ttg ctt ttc 385 Lys Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Val Leu Leu Phe 115 120 125	,
ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 130 135 140	,
ctg gac cag ggg aaa gtg tcc tcc att ttt tat act gcg gtg gtg ccc Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 145 150 155 160	-
atg ttt Met Phe	,
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Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ala Glu 35 40 45	
Thr Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu 50 55 60	
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val 65 70 75 80	
Thr Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 85 90 95	
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Ala Glu Gly Arg Ser	
100	

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 130 135 140

Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 145 150 150

Met Phe

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agc to Ser Cy	jc acc /s Thr	cta Leu 20	atg Met	ttg Leu	ggc Gly	tgc Cys	tta Leu 25	tgg Trp	acc Thr	act Thr	gcc Ala	agc Ser 30	ctc Leu	cat His	97
gcc ct Ala Le	t ctg eu Leu 35	cac His	acc Thr	ctt Leu	ctc Leu	ttg Leu 40	gcc Ala	cgg Arg	ctg Leu	gac Asp	ttc Phe 45	tgt Cys	gcc Ala	agc Ser	145
aat gt Asn Va	t atc al Ile )	ccc Pro	tac Tyr	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctc Leu	gtt Val	ccc Pro 60	ctg Leu	ctc Leu	cag Gln	ctc Leu	193
tcc to Ser Cy 65	gt tct ys Ser	gac Asp	acc Thr	cga Arg 70	ctc Leu	aac Asn	cag Gln	ctc Leu	atg Met 75	att Ile	gtg Val	ctg Leu	gtg Val	999 Gly 80	241
ggc ct	ig atc eu Ile	atc Ile	ctc Leu 85	ctg Leu	ccc Pro	ttc Phe	ctt Leu	ggc Gly 90	att Ile	ctc Leu	ggt Gly	tcc Ser	tac Tyr 95	aca Thr	289
tgc at Cys I	tt gca le Ala	gct Ala 100	gca Ala	gtg Val	ctc Leu	aga Arg	gtc Val 105	ccc Pro	tct Ser	gcc Ala	agg Arg	ggt Gly 110	acg Thr	tgg Trp	337
aag g Lys A	cc ttt la Phe 115	Ser	acc Thr	tgt Cys	ggc Gly	tcc Ser 120	cac His	ctg Leu	acc Thr	atg Met	gtc Val 125	atc Ile	ctc Leu	ttc Phe	385
Tyr G	gc acc ly Thr 30	atc Ile	tca Ser	ggg Gly	gtc Val 135	tac Tyr	ctg Leu	agg Arg	ccc Pro	tca Ser 140	tcc Ser	tcc Ser	cac His	tcc Ser	433
aca g Thr A	ac aag sp Lys	gac Asp	tca Ser	cta Leu	gcc Ala	tca Ser	gtg Val	atg Met	tac Tyr	atg Met	gta Val	gtg Val	acc Thr	ccc Pro	481

atg ctg Met Leu 487

<210> 302

<211> 162

<212> PRT

<213> Callithrix jacchus

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Ser Cys Thr Leu Met Leu Gly Cys Leu Trp Thr Thr Ala Ser Leu His 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Asp Phe Cys Ala Ser 35 40 45

Asn Val Ile Pro Tyr Phe Phe Cys Asp Leu Val Pro Leu Leu Gln Leu 50 55 60

Ser Cys Ser Asp Thr Arg Leu Asn Gln Leu Met Ile Val Leu Val Gly 65 70 75 80

Gly Leu Ile Ile Leu Leu Pro Phe Leu Gly Ile Leu Gly Ser Tyr Thr 85 90 95

Cys Ile Ala Ala Ala Val Leu Arg Val Pro Ser Ala Arg Gly Thr Trp

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Met Val Ile Leu Phe 115 120 125

Tyr Gly Thr Ile Ser Gly Val Tyr Leu Arg Pro Ser Ser His Ser 130 135 140

Thr Asp Lys Asp Ser Leu Ala Ser Val Met Tyr Met Val Val Thr Pro 145 150 155 160

Met Leu

<210> 303

<211> 487

<212> DNA

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<223> Product = olfactory receptor
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                                      10
ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat
                                                                       97
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
            20
tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac
                                                                      145
Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc atc cac ctt
                                                                      193
Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
    50
gcc tgt tct gac act ttt ctt aat gat gtg gtg atg tat ttg gcc gct
                                                                      241
Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
                                                                      289
gtg ctg ctg ggg ggt ggt ccc ctt gca ggg att ctt tac tct tac tct
Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser
                                                                      337
aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag tac
Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
                                105
            100
aag gca ttt tcc acc tgt gta tct cac atc tta att gtc tcc tta ttt
                                                                      385
Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe
                             120
tat ggt aca ctc cta ggt gtg tac ctt agt tct gct gca act ggc aac
                                                                      433
Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn
                         135
    130
                                                                      481
tca cat tca aga gct gca gcc tcg gtg atg tac act gtg gtc acc ccc
Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro
                                                             160
                                         155
                                                                      487
atg ctg
Met Leu
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<223> Taxon = 9483; gene = CJA197; Accession DDBJ/EMBL/GenBank = AF179807
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Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn 20 25 30

Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp 35 40 45

Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu 50 55 60

Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala 65 70 75 80

Val Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser 85 90 95

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
100 105 110

Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe 115 120 125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 130 135 140

Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

- <210> 305
- <211> 487
- <212> DNA
- <213> Callithrix jacchus
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- <222> (2)..(487)
- <223> Product = olfactory receptor
- <400> 305
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  Ile Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His

1				5					10					15	i	
ttc Phe	tgc Cys	ttc Phe	cgg Arg 20	ctc Leu	aca Thr	gtg Val	gga Gly	gtt Val 25	tac Tyr	att Ile	tta Leu	ggc Gly	atc Ile 30	ctt Leu	gga Gly	97
tct Ser	aca Thr	att Ile 35	cac His	acc Thr	agc Ser	tct Ser	atg Met 40	ttg Leu	aga Arg	ctc Leu	ttt Phe	ctg Leu 45	tgc Cys	aaa Lys	act Thr	145
aat Asn	gtg Val 50	att Ile	aac Asn	cat His	tat Tyr	ttt Phe 55	tgt Cys	gat Asp	ctc Leu	ttc Phe	.cct Pro 60	ctc Leu	ttg Leu	gaa Glu	ctc Leu	193
tcc Ser 65	tgc Cys	tcc Ser	agt Ser	acc Thr	tac Tyr 70	atc Ile	aat Asn	gaa Glu	tta Leu	cta Leu 75	gtt Val	ctg Leu	gtc Val	ttg Leu	agt Ser 80	241
gca Ala	ttg Leu	aat Asn	atc Ile	ctg Leu 85	acg Thr	cct Pro	gcc Ala	tta Leu	act Thr 90	atc Ile	ctg Leu	gcc Ala	tct Ser	tat Tyr 95	atc Ile	289
ttc Phe	acc Thr	att Ile	gcc Ala 100	Ser	atc Ile	ctc Leu	cac His	att Ile 105	ALG	tcc Ser	act Thr	gag Glu	ggc Gly 110		tcc Ser	337
aaa Lys	gcc Ala	ttc Phe 115	Ser	act Thr	tgc Cys	agc Ser	tcc Ser 120	urs	atc Ile	tca Ser	gct Ala	gtt Val 125		gtc Val	ttc Phe	385
ttt Phe	gga Gly	Ser	gca Ala	a gca a Ala	tto Phe	atg Met	Tyr	cto Lev	g cag Glr	g cca n Pro	tca Ser 140		gto Val	agt Ser	tcc Ser	433
ato Met	: Asr	caç Glr	g Gly	g aaa y Lys	gtg Val	. ser	tct Sei	gto Val	g ttt L Phe	tac Tyr 155		a act	gtt Val	gto L Val	g ccc l Pro 160	481 .
_	g cto Lev															487
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	00>															
I1 1	e Al	a Il	e Cy	rs Se 5	r Pr	o Le	u Le	eu Ty	r As	n Va	1 11	e Me	et S∈	er Ty 15	r His	
Pł	ne Cy	rs Ph	ne Ar 20	cg Le	eu Th	ır Va	ıl Gl	Ly Va 25	al T) 5	/r Il	e Le	eu Gi	ly I] 30	le Le	eu Gly	
Se	er Th	nr II 35		is Tl	nr Se	er Se	er Me	et Lo	eu A	rg Le	eu Pl	ne Le 4	eu Cy 5	ys L	ys Thr	

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Asn Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu
Ser Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser
Ala Leu Asn Ile Leu Thr Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile
                                     90
Phe Thr Ile Ala Ser Ile Leu His Ile Arg Ser Thr Glu Gly Arg Ser
                                 105
                                                     110
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ser Ala Val Ala Val Phe
Phe Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser
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Met Asp Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Thr Val Val Pro
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Met Leu
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                                        10
 tta tgc tgt gtg ttg gtt gct gcc tcc tgg atg gga gga ttt gtg cac
                                                                         97
 Leu Cys Cys Val Leu Val Ala Ala Ser Trp Met Gly Gly Phe Val His
                                                                        145
 tee ace gte cag ace att etc act ate egt etg ece ttt tgt ggg eca
 Ser Thr Val Gln Thr Ile Leu Thr Ile Arg Leu Pro Phe Cys Gly Pro
 aat cag gtg gac aac ttt ttt tgt gat gtt ccc cct gtc atc aaa ctt
                                                                        193
 Asn Gln Val Asp Asn Phe Phe Cys Asp Val Pro Pro Val Ile Lys Leu
                          55
     50
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gcc tgt gct gac act ttt gtc att gaa ttg ctc atg gta tct aac agt

Ala 65	Cys	Ala	Asp	Thr	Phe 70	Val	Ile	Glu	Leu	Leu 75	Met	Val	Ser	Asn	Ser 80		
gly ggg	ttg Leu	atc Ile	tcc Ser	acc Thr 85	agc Ser	tcc Ser	ttt Phe	gtg Val	gtg Val 90	ctg Leu	att Ile	tcc Ser	tcc Ser	tac Tyr 95	acc Thr		289
act Thr	atc Ile	cta Leu	gtc Val 100	aag Lys	att Ile	cac His	tcc Ser	aag Lys 105	gag Glu	gga Gly	agg Arg	cga Arg	aag Lys 110	gca Ala	ctc Leu		337
tcc Ser	aca Thr	tgt Cys 115	gcc Ala	tct Ser	cac His	ctt Leu	atg Met 120	gtg Val	gta Val	aca Thr	ctt Leu	ttt Phe 125	gga Gly	ccc Pro	tgt Cys		385
agt Ser	ttc Phe 130	atc Ile	tat Tyr	cct Pro	cat His	cct Pro 135	ttc Phe	tct Ser	aca Thr	ttt Phe	tct Ser 140	gtg Val	gac Asp	aag Lys	atg Met		433
gtg Val 145	tct Ser	gta Val	ctc Leu	tac Tyr	aag Lys 150	gtt Val	att Ile	act Thr	cca Pro	atg Met 155	cta Leu						469
<21 <21 <21 <21	1 > 2 >	308 156 PRT Call	ithr	ix j	acchi	us											
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Val 1	Ala	Ile	Cys	His 5	Pro	Leu	His	Tyr	Thr 10	Thr	Val	Met	Ser	Arg 15	Gly		
Leu	. Cys	Cys	Val	Leu	. Val	Ala	Ala	Ser 25	Trp	Met	Gly	Gly	Phe 30	Val	His		
Ser	Thr	Val	. Gln	Thr	: Ile	Leu	Thr 40	Ile	e Arg	, Lev	Pro	Phe	: Cys	Gly	Pro		
Asn	Glr 50	ı Val	. Asp	) Asr	n Phe	Phe 55	e Cys	a Asp	o Val	. Pro	Pro 60	val	Ile	. Lys	: Leu		
Ala 65	a Cys	s Ala	a Asp	Th:	? Phe	e Val	Ile	e Glu	ı Leı	ı Leı 75	ı Met	. Val	Ser	Asr	ser 80		
Gly	/ Let	ı Ile	e Sei	Th:	r Sei	: Sei	r Phe	e Val	l Va:	l Leı	ı Ile	e Ser	s Ser	туі 95	Thr		
Thi	r Ile	e Lei	ı Val		s Ile	e His	s Sei	Ly:		ı Gl	y Arg	g Arg	J Lys 11(	s Alá	a Leu		
Se	r Th:	r Cy:		a Se	r His	s Lei	u Met 120	z Va	l Va	l Th	r Le	u Phe 12!	e Gly 5	y Pro	o Cys		

## Ser Phe Ile Tyr Pro His Pro Phe Ser Thr Phe Ser Val Asp Lys Met 130 Val Ser Val Leu Tyr Lys Val Ile Thr Pro Met Leu 150 <210> 309 <211> 488 <212> DNA <213> Callithrix jacchus <220> <221> misc\_feature <222> (1)..(488) <223> Taxon = 9483; gene = CJA201; Accession DDBJ/EMBL/GenBank = AF179810 <220> CDS <221> (2)..(487) <222> Product = olfactory receptor <400> 309 c gtt gcc att tgc ttc ccc ctt cgc tat atg cta ctc atg agc cat tcc 49 Val Ala Ile Cys Phe Pro Leu Arg Tyr Met Leu Leu Met Ser His Ser att tgt gtc acg atg att ata gtt tgt tgg tcc att agc ata gct ggg 97 Ile Cys Val Thr Met Ile Ile Val Cys Trp Ser Ile Ser Ile Ala Gly 20 gcc ctg atc ctc act gtc ttc acc atg cat ctg cct tat tgt ggc ccc 145 Ala Leu Ile Leu Thr Val Phe Thr Met His Leu Pro Tyr Cys Gly Pro 40 35 tac aag ata aac cac ttc ttc tgt gag gtc cct gct gtc ctg aag ttg 193 Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu 50 gcc tgt gca gac aca tct ttt aat gac agg ctg gac ttc atc ttg ggt 241 Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly 75 70 ttc atc ctg ctt ttg gtc cca ctc tcc ctc atc ctg gcc tct tac gtc 289

Phe Ile Leu Leu Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Val

ttc atc ttt gcc tct atc ttc aga atc cgc tca gcg cag ggg agg ctc

Phe Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Ala Gln Gly Arg Leu

85

100

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<212> PRT

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<220>

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<222> (1)..(488)

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Ile Cys Val Thr Met Ile Ile Val Cys Trp Ser Ile Ser Ile Ala Gly

Ala Leu Ile Leu Thr Val Phe Thr Met His Leu Pro Tyr Cys Gly Pro

Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu

Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly 70

Phe Ile Leu Leu Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Val

Phe Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Ala Gln Gly Arg Leu 105

Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe

Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp

Pro Glu Arg Asp Lys Lys Leu Ala Leu Phe Tyr Asn Val Val Ser Gly 160 150

Phe Leu

<210> 311 <211> 487

<212> DNA

<213> Callithrix jacchus

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<221>
<222> (2)..(487)
<223> Product = olfactory receptor
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                                                                       49
 Val Ala Ile Cys His Pro Leu Arg Tyr Thr Ala Thr Met Asn Leu Arg
ctt tgt gtc cag cta gtg gct gga ctg tgg ctt gtt act tac ctc cat
                                                                       97
Leu Cys Val Gln Leu Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His
                                25
                                                                      145
gcc ctc ctg cat act tcc cta ata gca cat ctg tcc ttc tgt gcc ttc
Ala Leu Leu His Thr Ser Leu Ile Ala His Leu Ser Phe Cys Ala Phe
        3.5
aat atc atc cat cat ttc ttc tgt gat ctc aac cct cta cta cgg ctc
                                                                      193
Asn Ile Ile His His Phe Phe Cys Asp Leu Asn Pro Leu Leu Arg Leu
                        55
tet tge tet gee gte tee tte aac gta atg ate att ttt gea gta gga
                                                                      241
Ser Cys Ser Ala Val Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly
                    70
ggt cta ttg gct ctc acg ccc ctt gtc tgt atc ctc gta ttt tat gga
                                                                      289
Gly Leu Leu Ala Leu Thr Pro Leu Val Cys Ile Leu Val Phe Tyr Gly
                                     90
                                                                       337
ctt atc ttc tcc act gtt ctg aag atc acc tct act cag ggg aaa cag
Leu Ile Phe Ser Thr Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln
                                 105
            100
                                                                       385
aga gct gct tcc acc tgc ggc tgc cac ctg tca gta gtg gtg ctg ttt
Arg Ala Ala Ser Thr Cys Gly Cys His Leu Ser Val Val Leu Phe
                             120
                                                 125
tat gge aca gcc att gcc gtc tac ttt agc ccc tca tcc tcc cat acg
                                                                       433
Tyr Gly Thr Ala Ile Ala Val Tyr Phe Ser Pro Ser Ser His Thr
                         135
    130
cct gag agt gac act ctc tcg acc gtc atg tat tca gtg gtg gcc ccg
                                                                       481
 Pro Glu Ser Asp Thr Leu Ser Thr Val Met Tyr Ser Val Val Ala Pro
                                                              160
                                         155
 145
                                                                       487
 atg ctg
Met Leu
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Val 1	Ala	Ile	Cys	His 5	Pro	Leu	Arg	Tyr	Thr 10	Ala	Thr	Met	Asn	Leu 15	Arg
Leu	Cys	Val	Gln 20	Leu	Val	Ala	Gly	Leu 25	Trp	Leu	Val	Thr	Tyr 30	Leu	His
Ala	Leu	Leu 35	His	Thr	Ser	Leu	Ile 40	Ala	His	Leu	Ser	Phe 45	Cys	Ala	Phe
Asn	Ile 50	Ile	His	His	Phe	Phe 55	Cys	Asp	Leu	Asn	Pro 60	Leu	Leu	Arg	Leu
Ser 65	Cys	Ser	Ala	Val	Ser 70	Phe	Asn	Val	Met	Ile 75	Ile	Phe	Ala	Val	Gly 80
Gly	Leu	Leu	Ala	Leu 85	Thr	Pro	Leu	Val	Cys 90	Ile	Leu	Val	Phe	Tyr 95	Gly
Leu	Ile	Phe	Ser 100		Val	Leu	Lys	Ile 105	Thr	Ser	Thr	Gln	Gly 110	Lys	Gln
Arg	, Ala	Ala 115		Thr	Cys	Gly	Cys 120	His	Leu	Ser	Val	Val 125	Val	Leu	Phe
Туз	Gly		Ala	Ile	Ala	Val 135	Tyr	Phe	Ser	Pro	Ser 140	Ser	Ser	His	Thr
Pro	o Glu	Ser	Asp	Thr	Leu 150	Ser	Thr	Val	Met	Tyr 155	Ser	Val	Val	Ala	Pro 160
Me	. Leu	ı													
<2 <2	10> 11> 12> 13>	313 491 DNA Pong	do b?	/gmae	eus										

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cctttcactg ggtgtctatg ggatgggggt ttttgggggct gtggttcata tgggaaacat	120
aatgtttatg teettttgtg gagacaaeet tgteaateae tatetgtgtg acateettee	180
tctccttgag ctctcctgca acagctctta cataaatttg ctggtggttt ttattattgt	240

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gaccattggc attggggtgc caattgtcac catttttatc tcttatggtt ttattctttc
                                                                     300
cagcattete cacattaget cacagaggge aggteaggte taaageette agtaeetgea
                                                                     360
gttcccacat aattgtggta tcgcttttct ttgggtcagg tgctttcatg tacctcaaac
                                                                     420
caccttctct tctacccctg gaccagggga aagtgtcctc cattttttat actgctgtgg
                                                                     480
                                                                     491
tqcccatqtt t
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      314
      480
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                                                                       60
cccttttggc gctgtcctgg gtgctgacca ccttccatgc catgttacac actttactca
                                                                      120
tggccaggtt gtgtttttgt gcagacaatg tgatccccca ctttttctgt gatatgtctg
                                                                      180
ctctgctgaa gctgtcctgc tctgacactc gagttaatga attggtgata tttatcatgg
                                                                      240
gagggctcat tcttgtcatc ccattcctac tcatccttgg gtcctatgca cgaattgtct
                                                                      300
cetecateet caaggteest tetaagggta tetgeaagge ettetetaet tgtggeteee
                                                                      360
acctctctgt ggtgtccctg ttctatggga ccgttagtgg tctctactta tgcccatcgg
                                                                      420
ctaatagttc tactctgaag gagactgtca tggctgtaat gtacactgtg gtgaccccca
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<211> 486
 <212> DNA
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 Cys Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
 cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt
                                                                        96
 Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
                                 25
 gct ctt ttg cat acc ctc ctt ctg gcc cgg ctt tcc ttc tgt gct gac
                                                                       144
 Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
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		35					40					45						
cac His	atc Ile 50	atc Ile	tct Ser	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu		1	.92
tcc Ser 65	tgc Cys	tca Ser	gac Asp	acc Thr	tcc Ser 70	ctc Leu	aat Asn	cag Gln	tta Leu	gca Ala 75	atc Ile	ttt Phe	aca Thr	gca Ala	gga Gly 80		2	240
ttg Leu	aca Thr	gcc Ala	att Ile	atg Met 85	ctt Leu	cca Pro	ttc Phe	ctg Leu	tgc Cys 90	atc Ile	ctg Leu	gtt Val	tct Ser	tat Tyr 95	ggt Gly		2	288
cac His	att Ile	Gly ggg	gtc Val 100	acc Thr	atc Ile	ctc Leu	cag Gln	att Ile 105	ccc Pro	tcc Ser	acc Thr	aag Lys	ggc Gly 110	ata Ile	tgc Cys		3	336
aaa Lys	gcc Ala	ttg Leu 115	tcc Ser	act Thr	tgt Cys	gga Gly	tcc Ser 120	cac His	ctc Leu	tca Ser	gtg Val	gtg Val 125	act Thr	atc Ile	tat Tyr		3	384
tat Tyr	999 Gly 130	aca Thr	att Ile	att Ile	ggt Gly	ctc Leu 135	tat Tyr	ttt Phe	cta Leu	ccc Pro	cca Pro 140	tcc Ser	agc Ser	aac Asn	acc Thr		4	132
aat Asn 145	gac Asp	aag Lys	aac Asn	ata Ile	att Ile 150	gct Ala	tca Ser	gtg Val	ata Ile	tac Tyr 155	aca Thr	gta Val	gtc Val	act Thr	ccc Pro 160		4	480
	ttg Leu																.*	486
<21 <21 <21 <21	1 > 2 >	316 162 PRT Pong	о ру	gmae	us													
<22 <22 <22 <22	1>	misc (1). Taxo	_ (48	6)		ne =	PPY	112;	Acc	essi	on D	DBJ/	EMBL	/Gen	Bank	= <i>P</i>	\F1	79814
<40	0>	316																
Cys 1	Ala	Ile	Cys	His 5	Pro	Leu	His	Tyr	Ala 10	Thr	Ile	Met	Ser	Gln 15	Ser			
Gln	Cys	Val	Met 20	Leu	Val	Ala	Gly	Ser 25	Trp	Val	Ile	Ala	Cys 30	Ala	Cys			
Ala	Leu	Leu 35	His	Thr	Leu	Leu	Leu 40	Ala	Arg	Leu	Ser	Phe 45	Cys	Ala	Asp			
His	; Il∈ 50	: Ile	Ser	His	Phe	Phe	. Cys	Asp	Leu	Gly	Ala	Leu	Leu	Lys	Leu			
Ser 65	Сув	s Ser	Asp	Thr	Ser 70	Leu	ı Asr	Glr.	Leu	Ala 75	Ile	Phe	Thr	Ala	Gly 80			

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Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
                                105
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
                                                             160
                    150
Met Leu
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<222>
= AF179815
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cactgccatt tgccaccctc taagataaac caatctcatg agacccaaaa tttgtggact
                                                                       60
tatgactgcc ttctcctgga tcctgggctc tacggatgga atcattgatg ctgcagcgac
                                                                      120
 attttccttc tcctactgtg ggtctcggga aatagcccac ttcttctgtg agttcccttc
                                                                       180
 catactaatc ctctcatgca atgacacatc aatatttgaa aaggttcttt tcatctgctg
                                                                      240
 tatagtaatg attgtttttc ctgttgcaat catcatcgct tcctatgctc aagttattct
                                                                       300
 ggctgtcatt cacatgggat ctggagaggg tcgtcggata gctttcacga cctgttcctc
                                                                       360
 tcacctcatg gtggtgggaa tgtactatgg agcagctttg ttcatgtaca tacggcccac
                                                                       420
 atctgatcgc tcccctacac aggacaagat ggtgtctgta ttctacacca tcctcactcc
                                                                       480
                                                                       487
 catgctg
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        318
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        484
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        DNA
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<222> (2)..(484)
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                                                                          49
 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
ctc tgt ctc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
                                                                          97
Leu Cys Leu Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                                                                         145
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac
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aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
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Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
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Ser Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
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ggg ctc att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca
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Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
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                                                                         337
cga att gtc tcc tcc atc ctc aag gtc cct tct aag ggt atc tgc aag
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys
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ged the tet act tgt ggd ted cac etc tet gtg gtg ted etg tte tat
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Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
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Gly Thr Val Ser Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr
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Ser Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
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Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys
Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
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96
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tgt Cys 65	gtg Val	gac Asp	gtc Val	tcc Ser	ttc Phe 70	aac Asn	aag Lys	gcc Ala	atg Met	gtg Val 75	gcc Ala	atc Ile	tca Ser	gly aaa	ttt Phe 80		240
ctg Leu	gtg Val	atc Ile	ctg Leu	ctt Leu 85	ccc Pro	tgt Cys	tca Ser	ctg Leu	atc Ile 90	cta Leu	ttc Phe	tcc Ser	tat Tyr	gct Ala 95	cac His		288
ata Ile	gtt Val	gct Ala	gcc Ala 100	att Ile	ctt Leu	cat His	att Ile	cct Pro 105	tct Ser	gcc Ala	cag Gln	gga Gly	cgc Arg 110	cgc Arg	aaa Lys		336
gcc Ala	ttt Phe	999 Gly 115	act Thr	tgc Cys	acg Thr	tct Ser	cac His 120	ctc Leu	act Thr	gtg Val	gtt Val	tgc Cys 125	atg Met	tgc Cys	ttt Phe		384
gly aaa	gct Ala 130	aca Thr	atg Met	ttc Phe	acc Thr	tac Tyr 135	atg Met	aga Arg	cct Pro	gcg Ala	ggc Gly 140	ggc Gly	tcc Ser	tcc Ser	ctg Leu		432
gaa Glu 145	Lys	aag Lys	aat Asn	atg Met	gtt Val 150	gcc Ala	ctc Leu	ttt Phe	tat Tyr	gcc Ala 155	att Ile	gtg Val	att Ile	cca Pro	atg Met 160		480
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Lei	u Cys	s Lev	1 Gly 20	, Lei	ı Val	Ala	Gly	7 Cys 25	s Leu	ı Val	l Ala	a Gly	7 Phe 30	e Met	Asn		
Se	r Lei	ı Met 35	: Glu	ı Thi	c Ile	e Ile	Thi 40	r Phe	e Glr	ı Leı	ı Lev	ı Let 45	ı Cys	s His	s Asn		
Va	1 Il 50	e Ası	n Hi:	s Phe	e Ala	a Cys 55	s Glı	ı Th:	r Lei	ı Ala	a Va:	l Lei	ı Arg	g Lei	ı Ala		
Су 65		l As	ρ Va.	l Se	r Pho	e Ası	n Ly:	s Al	a Me	t Va 75	l Ala	a Il	e Se	r Gl	y Phe 80		

Leu	Val	Ile	Leu	Leu 85	Pro	Cys	Ser	Leu	Ile 90	Leu	Phe	Ser	Tyr	Ala 95	His	
Ile	Val	Ala	Ala 100	Ile	Leu	His		Pro 105	Ser	Ala	Gln	Gly	Arg 110	Arg	Lys	
Ala	Phe	Gly 115	Thr	Cys	Thr	Ser	His 120	Leu	Thr	Val	Val	Cys 125	Met	Cys	Phe	
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tcc Ser	cto Lei	g ato 1 Met 35	g gaa : Glu	aca Thr	att Ile	atc Ile	acc Thr 40	tto Phe	cag Glr	r ctt Lev	ccc Pro	cto Lev 45	g tgt L Cys	cac His	aat Asn	145
gtt Val	ati	aat	cac	ttt	gcc	tgt Cys	gag Glu	aco Thi	tta Lei	gca Ala	gto Val	g cta Lei	cga Arg	a cta g Lei	a gcc ı Ala	193
	. Ile	e Asr	n His	Pne	HIG	55					60					
Fat	50	a da	- atc	tco	· ++c	55 : aac	aac	ı acı	c acc	a ata	g gco	c ato	tca Se:	a ggg	g ttt y Phe 80	241

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gcc ttt ggg acc tgc acg tct cac ctc act gtg gtt tgc atg tgc ttt Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe 115 120 125	385
ggg gct aca atg ttc acc tac atg aga cct gcg ggt ggc tcc tcc ctg Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu 130 135 140	433
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ctt Leu	484
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Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Pro Leu Cys His Asn 35 40 45	
Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala 50 55 60	
Cys Val Asp Val Ser Phe Asn Lys Ala Thr Val Ala Ile Ser Gly Phe 65 70 75 80	,
Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His 85 90 95	
Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Gln Gly His Arg Lys 100 105 110	
Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe 115 120 125	

Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu

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Glu Lys Glu Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met 145 150 155 160

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                                                                      180
gagtgaccaa acttgcctgc ctggactctt acctcattga aatactaatt gtggtcaata
                                                                      240
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atattgcagt agtaatatta ttctttggac cttgcatctt catctatgtg tggcccttta
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cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt
                                                                       97
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
gct ctt ttg cat acc ctc ctt ctg gcc cgg ctt tcc ttc tgt gct gac
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Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp

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tcc Ser 65	tgc Cys	tca Ser	gac Asp	acc Thr	tcc Ser 70	ctc Leu	aat Asn	cag Gln	tta Leu	gca Ala 75	atc Ile	ttt Phe	aca Thr	gca Ala	gga Gly 80		241
ttg Leu	aca Thr	gcc Ala	att Ile	atg Met 85	ctt Leu	cca Pro	ttc Phe	ctg Leu	tgc Cys 90	atc Ile	ctg Leu	gtt Val	tct Ser	tat Tyr 95	ggt Gly		289
cac His	att Ile	ggg ggg	gtc Val 100	acc Thr	atc Ile	ctc Leu	cag Gln	att Ile 105	ccc Pro	tcc Ser	acc Thr	aag Lys	ggc Gly 110	ata Ile	tgc Cys		337
aaa Lys	gcc Ala	ttg Leu 115	tcc Ser	act Thr	tgt Cys	gga Gly	tcc Ser 120	cac His	ctc Leu	tca Ser	gtg Val	gtg Val 125	act Thr	atc Ile	tat Tyr		385
tat Tyr	ggg Gly 130	aca Thr	att Ile	att Ile	ggt Gly	ctc Leu 135	tat Tyr	ttt Phe	ctt Leu	ccc Pro	cca Pro 140	tcc Ser	agc Ser	aac Asn	acc Thr		433
aat Asn 145	gac Asp	aag Lys	aac Asn	ata Ile	att Ile 150	gct Ala	tca Ser	gtg Val	ata Ile	tac Tyr 155	aca Thr	gta Val	gtc Val	act Thr	ccc Pro 160		481
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Glr	суя	. Val	Met 20	: Leu	ı Val	Ala	a Gly	7 Sei 25	Trp	val	. Il€	e Ala	a Cys 30	s Ala	a Cys		
Ala	ı Lev	Leu 35	n His	s Thi	: Leu	ı Let	ı Let 40	ı Ala	a Arg	g Let	ı Sei	c Phe 45	е Сув	s Ala	a Asp		
His	: Ile	e Ile	e Sei	His	s Phe	Phe	e Cys	a Ası	p Let	ı Gly	Ala	a Let	ı Leı	ı Lyı	s Leu		

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80

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His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
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Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
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                                                                      300
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tgtgcagcga cattcctcag caggtatggc caaggctcac agcactctga ctgcccacat
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tgctgtggtg accgtgttct ttgggccctg tatcttcatc tatgcctggc ctttcagcaa
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  cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt
                                                                            97
  Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
  gct ctt ttg cat acc ctc ctt ctg gcc cgg ctt tcc ttc tgt gct gac
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  Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
  cac atc atc cct cac ttc ttc tgc gac ctt ggt gcc ctg ctc aag ctg
                                                                           193
  His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
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  tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga
                                                                           241
  Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
  ttg aca gcc att atg ctt cca ttc ctg tgc atc ctg gtt tct tat ggt
                                                                           289
  Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
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  cac att ggg gtc acc atc ctc cag att ccc tcc acc aag ggc ata tgc
                                                                           337
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Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
                                                                           385
                                120
  tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc
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  Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
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  aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc
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His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 120

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Product = olfactory receptor

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145 tee ete tet cae ace ett etg etg ace eeg etg eet tte tgt gat gea Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Pro Phe Cys Asp Ala 40 35

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60	193										
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gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95	289										
tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100 105 110	337										
aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr 115 120 125	385										
tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135	433										
att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 155	481										
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Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
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Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
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                                                                       97
ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
                                25
                                                                      145
 tee etc tet cae ace ett etg etg ace eeg etg tet tte tgt gat gea
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
                                                                      193
 aac acc gtc cac cac tac ttc tgt gac ctt gct gcc ctg ctc aag ctg
 Asn Thr Val His His Tyr Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
    50
                                                                      241
 tee tge tea gat ate tte ete aac gag etg gte atg tte aca gta ggg
 Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
                                                                      289
 gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc
 Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
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90

tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg

aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat 385 Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc 433 Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 135 att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 481 150 488 atg ctg t Met Leu

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Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser 25 20

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala 35

Asn Thr Val His His Tyr Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly

Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 90

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser 135 130

Ile	Asp	Lys	Asp	Val	Ile	Val	Ala	Leu	Met	Tyr	Thr	Val	Val	Thr	Pro
145					150					155					160

Met Leu

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  Val Ala Thr Cys His Pro Leu Arg Tyr Met Val Ile Met Asn Pro Cys
                                                                              97
ctc tgc agc ctg ctg att ctt ctt tct ccg ttg act agc gtt gtg aat
Leu Cys Ser Leu Leu Ile Leu Leu Ser Pro Leu Thr Ser Val Val Asn
gcc ctt ctt ctc agc ctg atg gtg ttg agg ctg tcc ttc tgc aca gat
Ala Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp
                                                                            145
ctg gaa atc ccg ctc ttc ttc tgt gaa ctg gct cag gtc atc cag ctt
                                                                             193
Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu
                          55
gct tgt tct gac acc ctc atc aat aac atc ctg ata tat ttt gca gct
                                                                             241
Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala
                      70
tgc ata ttt ggt ggt gtt cct ctg tct gga atc ata ttc tct tat gct
                                                                             289
Cys Ile Phe Gly Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ala
                                        90
cag att gcc tcc tct att ttg aga atg cca tca gca cgc aga aag tat
                                                                             337
Gln Ile Ala Ser Ser Ile Leu Arg Met Pro Ser Ala Arg Arg Lys Tyr
aaa gcc ttt tcc acc tgt ggg tct cac ctc tcc atg gtg ctc ttg ttc
                                                                             385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Met Val Leu Leu Phe
                               120
tat agg aca ggt ttg ggg gtg tac att agt tct gca gtt act gac tca
                                                                             433
Tyr Arg Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser
cct agg aag act gca gtg gct tca atg atg tat tct gtg ggt cct caa
Pro Arg Lys Thr Ala Val Ala Ser Met Met Tyr Ser Val Gly Pro Gln
                                                                             481
                                            155
145
                                                                             487
atg gtg
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             20
Ala Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp
                              40
         35
Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu
                          55
    50
Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala
Cys Ile Phe Gly Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ala
                                       90
Gln Ile Ala Ser Ser Ile Leu Arg Met Pro Ser Ala Arg Arg Lys Tyr
                                                         110
                                   105
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Met Val Leu Leu Phe
                               120
         115
 Tyr Arg Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser
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 Pro Arg Lys Thr Ala Val Ala Ser Met Met Tyr Ser Val Gly Pro Gln
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                      150
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 Met Val
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  Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
ctg tct cgc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
                                                                          97
Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
            2.0
gcc atg ttg cac act tta ctc atg gcc agg ttg cgt ttt tgt gca gac
                                                                         145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Arg Phe Cys Ala Asp
                             40
aat gtg atc ctc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
                                                                         193
Asn Val Ile Leu His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
                         55
gcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga
                                                                         241
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
                                          75
ggc ctc att ctt gtc atc cca ttt cta ctt atc att ggg tcc tac gca
                                                                         289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
cga att gtc ttc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc
                                                                         337
Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
                                  105
aag gcc gtc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc
                                                                         385
Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
                              120
         115
tat ggg act gtt att ggt ctc tac tta tgc cca tca gct aat aat tct
                                                                          433
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
act cta aag gag act gtc atg gct gtg atg tac act gtg atg gcc ccc
Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
                                                                          481
                                          155
                      150
                                                                          487
 atg ctg
Met Leu
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Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Arg Phe Cys Ala Asp
Asn Val Ile Leu His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
                            120
        115
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
                        135
Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
                    150
145
Met Leu
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aac Asn	gtc Val 50	gtt Val	gat Asp	cat His	ttc Phe	tac Tyr 55	ttt Phe	gac Asp	act Thr	atc Ile	ccg Pro 60	ctc Leu	ctg Leu	cag Gln	att Ile	193
tcc Ser 65	tgc Cys	aca Thr	gac Asp	acg Thr	cag Gln 70	ctc Leu	ctg Leu	gag Glu	agg Arg	atg Met 75	gga Gly	ttc Phe	atc Ile	tca Ser	gcg Ala 80	241
ttg Leu	gtg Val	aca Thr	ctc Leu	tta Leu 85	gtc Val	aca Thr	ttg Leu	gta Val	atg Met 90	gtg Val	ata Ile	ata Ile	tca Ser	tat Tyr 95	act Thr	289
tat Tyr	att Ile	gcc Ala	ctg Leu 100	aca Thr	att Ile	cta Leu	aaa Lys	atc Ile 105	cct Pro	tca Ser	act Thr	agt Ser	cag Gln 110	agg Arg	aaa Lys	337
aag Lys	gct Ala	ttt Phe 115	Ser	acg Thr	tgt Cys	tct Ser	tct Ser 120	cac His	atg Met	att Ile	gtg Val	ata Ile 125	tcc Ser	ctt Leu	tct Ser	385
tat Tyr	ggc Gly 130	Ser	tgc Cys	atc Ile	ttc Phe	atg Met 135	tat Tyr	gtt Val	aag Lys	cca Pro	tca Ser 140	gtc Val	aaa Lys	caa Gln	agg Arg	433
gta Val 145	Ser	ttt Phe	tca Ser	aag Lys	gga Gly 150	Ile	tcg Ser	gtg Val	ctc	aat Asn 155	Thr	tct Ser	gtt Val	gct Ala	cca Pro 160	481
	ttg Leu															487
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Val 1	L Ala	a Ile	е Суя	s Lys 5	s Pro	) Lei	ı Hi:	з Ту:	r Thi	r Thi	c Ile	e Met	: Sei	r Sei 15	. Lys	
Ile	е Су	s Le	u Gl: 20	n Lei	u Va	l Lei	u Gl	у Су 25	s Tr	p Vai	l Le	u Gl	y Pho 30	e Lei	ı Ile	
Ile	e Ph	e Pr		o Le	u Le	u Le	u Gl 40	y Le	u As	n Le	u As	p Pho 45	е Су	s Ala	a Ser	
As	n Va 50		l As	p Hi	s Ph	е Ту 55	r Ph	e As	p Th	r Il	e Pr 60	o Le	u Le	u Gl	n Ile	

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Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
                85
Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
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Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
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 tac tgt gga cag ctg gtg gct ttc tct tac atg agt ggt ttc atg atc
                                                                           96
Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile
             20
 tct gtc atc aag gtc tat ttc att tca cat gtt gct ttc tgt ggc tcc
Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser
                                                                          144
                               40
 aat gtt atg aac cac ttt ttc tgt gat atc tca cca gtc cta aaa ctg
                                                                          192
 Asn Val Met Asn His Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu
 gca tgc aaa gac atg tcc aca gct gag cta gtg gac ttt gct tta gct
                                                                          240
 Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala
                                           75
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atc gtc att ctt gtg atc cct ctc att acc act atc ctc tcc tat atc  Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile  85  90  95	88
tac att gtc tcc gcc att ctg cat ata ccc tcc acc cag gga agg aag Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys 100 105 110	36
aag gcc ttc tcc acc tgt gca tct cac ctc act gta gtc ata att ttt Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe 115 120 125	84
tac aca gcc atg att ttt aca tat gtt cgg ccc aga gct att gca tca Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser 130 135 140	32
ttt aat tcc aac aaa cta atg tca gct gtg tat gca gtc ctc aca ccc Phe Asn Ser Asn Lys Leu Met Ser Ala Val Tyr Ala Val Leu Thr Pro 145 150 155 160	80
atg ct Met	85
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<pre>&lt;222&gt; (1)(485) &lt;223&gt; Taxon = 9521; gene = SSC191; Accession DDBJ/EMBL/GenBank = AF17 &lt;400&gt; 341  Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly 15</pre>	79828
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115 120 125

Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser . 130  $\,$  135  $\,$  140  $\,$ 

Phe Asn Ser Asn Lys Leu Met Ser Ala Val Tyr Ala Val Leu Thr Pro 145 150 150

Met

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tcc ctc tct cac acc ctt ctg ctg acc ccg ctg tct ttc tgt gat gca Ser Leu Ser His Thr Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala 35 40 45	45
aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60	93
tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80	41
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95	89
tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100 105 110	37
aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat  Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr  115 120 125	85
tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 140	33

Met Leu

att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 155 160	181
atg ctg Met Leu	487
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Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60	
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80	
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95	
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100 105 110	
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr 115 120 125	
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 140	
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                                                                        97
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
tee etc tet cac acc ett etg etg acc eeg etg tet tte tgt gat gea
                                                                       145
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
                                                                       193
aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
                        55
                                                                       241
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Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
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gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc
                                                                       289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
tac act ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cgc
                                                                       337
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
                                 105
aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat
                                                                       385
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
                                                  125
                             120
tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc
                                                                        433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
                                                                        481
att gac aag gat gtc att gtg gct cta acg tac aca gtg gtc aca ccc
Ile Asp Lys Asp Val Ile Val Ala Leu Thr Tyr Thr Val Val Thr Pro
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145
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Met Leu
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         35
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
     50
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
                     70
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                                      90
 Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
                                                      110
 Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
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 Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser
 Ile Asp Lys Asp Val Ile Val Ala Leu Thr Tyr Thr Val Val Thr Pro
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 Met Leu
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ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn 20 25 30	97
tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp 35 40 45	145
ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc ata cat ctt Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu 50 55 60	193
gcc tgt tat gac act ttc ctt aat gat gtg gtg atg tat ttg gca gct Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala 65 70 75 80	241
atg ctg ctg ggc ggt ggt ccc ctc aca gga att att tac tct tac tct Met Leu Leu Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser 85 90 95	289
aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag tac Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr 100 105 110	337
aag gcg ttt tcc acc tgt gca tct cac atc tta att gtc tcc tta ttt Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe 115 120 125	385
tat ggt aca ctc cta ggt gtg tac att agt tct gct gca act ggc aac Tyr Gly Thr Leu Leu Gly Val Tyr Ile Ser Ser Ala Ala Thr Gly Asn 130 135 140	433
tca cat tca agt gct gca gcc ttg gtg atg tac act gtg gtc acc ccc Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro 145 150 155 160	481
atg ct Met	486
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Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn 20 25 30





Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp 40

Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu

Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala

Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr 105

Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe 120 115

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Met

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gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt tca gaa 145 Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu 45

aat ctt gtc aat cac tac atg tgt gat gtc ctt ccc ctc ctt gag ctc 193 Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu

241 tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt 289 Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 90 85 ttt att ctt tcc agc att ctc cac att agc tcc aca gag ggc agg tct 337 Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser 105 385 aaa gcc ttc agt acc tgc agc tcc cac ata att gtg gta tcg ctt ttc Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe 125 115 ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 433 135 130 ctg gac cag ggg aaa gtg tct tcc att ttt tat act gca gtg gtg ccc 481 Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 155 150 487 atg ttt Met Phe <210> 349 <211> 162 <212> PRT <213> Saimiri sciureus <220> <221> misc\_feature (1)...(487)<222> Taxon = 9521; gene = SSC195; Accession DDBJ/EMBL/GenBank = AF179832 <223> <400> 349 Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu 35 Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu 50

Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val 65 70 75 80

Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 85 90 95

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Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
                                105
           100
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
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Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
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Met Phe
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                                                                     120
cetecatatt cectactgea ggtetagage cattgaceat ttettetgeg acateceage
                                                                     180
catgttgctt ctcgcctgta cggacacttg ggtctatgaa tacatggttt ttctaagtac
                                                                     240
aagctgcctt ctcctctttc tttccttggc atcaccgctt cctatggccg agtcctattt
                                                                     300
gctgtctacc atacgcattc aaaaaaggga agaaaaaagg cctccaccac catttcaacc
                                                                     360
catttaactg tagtgatctt ttactatgca ccttttgtct acacctatct tcggcccagg
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aatctccact caccatccga agacaagatc ctggcagtct tctacaccat ccttacccct
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atc tgc c Ile Cys I	ctg cag Leu Gln 20	ctt gt Leu Va	g ctt l Leu	ggg Gly	tgc Cys 25	tgg Trp	gtt Val	ctt Leu	ggt Gly	ttt Phe 30	ctc Leu	atc Ile	97
atc ttt c Ile Phe E	cca cca Pro Pro 35	ctc ct Leu Le	c tta u Leu	gga Gly 40	cta Leu	aat Asn	ctt Leu	gac Asp	ttc Phe 45	tgt Cys	gcc Ala	tcc Ser	145
aac gtc g Asn Val V 50	gtt gat Val Asp	cat tt His Ph	c tac e Tyr 55	tgt Cys	gac Asp	act Thr	atc Ile	ccg Pro 60	ctc Leu	ctg Leu	cag Gln	att Ile	193
tcc tgc a Ser Cys 7 65	aca gac Thr Asp	acg ca Thr Gl	n Leu	ctg Leu	gag Glu	agg Arg	atg Met 75	gga Gly	ttc Phe	atc Ile	tca Ser	gcg Ala 80	241
ctg gtg a	aca ctc Thr Leu	tta gt Leu Va 85	c aca l Thr	ttg Leu	gta Val	atg Met 90	gtg Val	ata Ile	ata Ile	tca Ser	tat Tyr 95	act Thr	289
tat att o	gcc ctg Ala Leu 100	aca at Thr Il	t cta e Leu	aaa Lys	atc Ile 105	cct Pro	tca Ser	act Thr	agt Ser	cag Gln 110	agg Arg	aaa Lys	337
aag gct i Lys Ala i	ttt tcc Phe Ser 115	acg to	t tct s Ser	tct Ser 120	cac His	atg Met	att Ile	gtg Val	ata Ile 125	tcc Ser	ctt Leu	tct Ser	385
tat ggc Tyr Gly 130	agc tgc Ser Cys	atc tt Ile Ph	c atg e Met 135	Tyr	gtt Val	aag Lys	cca Pro	tca Ser 140	gtc Val	aaa Lys	caa Gln	agg Arg	433
gta tct Val Ser 145	ttt tca Phe Ser	aag gg Lys G	y Ile	tcg Ser	gtg Val	ctc Leu	aat Asn 155	acc Thr	tct Ser	gtt Val	gct Ala	cca Pro 160	481
ctt ttg Leu Leu													487
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Ile Cys	Leu Glr 20	ı Leu V	al Le	ı Gly	7 Cys 25	Trp	Val	. Leu	ı Gly	Phe 30	e Leu	ılle	

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Ile Phe Pro Pro Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser
Asn Val Val Asp His Phe Tyr Cys Asp Thr Ile Pro Leu Leu Gln Ile
                        55
Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
                                                        95
Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
                                105
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
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Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
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Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
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Leu Leu
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  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Leu Leu Met Ser His Ser
                                                                       97
att tgt gtc aac acg gtc att gtc tgt tgg tcc att agc ata gct ggg
Ile Cys Val Asn Thr Val Ile Val Cys Trp Ser Ile Ser Ile Ala Gly
            20
gcc ctg atc tac act gtc ttc acc ttg cat ctg cct tat tgt ggc ccc
                                                                      145
Ala Leu Ile Tyr Thr Val Phe Thr Leu His Leu Pro Tyr Cys Gly Pro
                            40
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tac aag ata aac cac ttc ttc tgt gag gtc cct gct gtc ctg aag ttg

Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu 50 55 60	Lys Leu
gcc tgt gca gac aca tct ttt aat gac agg ctg gac ttc att Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile 65 70 75	ttg ggt 241 Leu Gly 80
ttc ctc ctg ctt ttg gtc cca ctc tcc ttc atc ctg gcc tct Phe Leu Leu Leu Val Pro Leu Ser Phe Ile Leu Ala Ser 85 90	tac gta 289 Tyr Val 95
ctc atc ttt gcc tct atc ttc aga atc cgc tca gtg cag ggg Leu Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Val Gln Gly 100 105 116	Arg Leu
aag too tto too acg tgt got too cac gto act gtg gto acc Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr 115 120 125	e atg ttc 385 Met Phe
tac gga ccg gcc atc atc atg tac atg agg ccc ggt tct tgg Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Try 130 135 140	g tat gac 433 o Tyr Asp
cca gag tgg gac aag aag gta gag gtg ttg tac aat gtc atc Pro Glu Trp Asp Lys Lys Val Glu Val Leu Tyr Asn Val Ile 145 150 155	e tet gee 481 e Ser Ala 160
ttc ttg Phe Leu	487
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Ile Cys Val Asn Thr Val Ile Val Cys Trp Ser Ile Ser Il 20 25 30	e Ala Gly
Ala Leu Ile Tyr Thr Val Phe Thr Leu His Leu Pro Tyr Cy 35 40 45	s Gly Pro
Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Le 50 55 60	u Lys Leu
Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Il 65 70 75	e Leu Gly 80
Phe Leu Leu Leu Val Pro Leu Ser Phe Ile Leu Ala Se	

1	Leu	Ile	Phe	Ala 100	Ser	Ile	Phe	Arg	Ile 105	Arg	Ser	Val	Gln	Gly 110	Arg	Leu	
1	Lys	Ser	Phe 115	Ser	Thr	Сув		Ser 120	His	Val	Thr	Val	Val 125	Thr	Met	Phe	
5	Tyr	Gly 130	Pro	Ala	Ile	Ile	Met 135	Tyr	Met	Arg	Pro	Gly 140	Ser	Trp	Tyr	Asp	
	Pro 145	Glu	Trp	Asp	Lys	Lys 150	Val	Glu	Val	Leu	Tyr 155	Asn	Val	Ile	Ser	Ala 160	
:	Phe	Leu															
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	gcc Ala	tgo Cys	atg Met	acc Thr	atg Met	gtg Val	ggc	acc Thr	tcc Ser 25	tgg Trp	ctc Leu	aca Thr	ggc	ato Ile 30	ato Ile	aca Thr	97
	gcc Ala	aco Thi	acc Thr	cat His	gcc Ala	tcc Ser	ctc Leu	atc Ile 40	ttc Phe	tct Ser	ctg Leu	cc,c Pro	ttc Phe 45	ccc Pro	ago Ser	cac His	145
	cca Pro	ate Met	g ato	c cca e Pro	cac His	ttt Phe	ctc Leu 55	tgt Cys	gac Asp	atc Ile	ctg Leu	cca Pro 60	gta Val	ctg Leu	g aga ı Arg	a ctg g Leu	193
	gca Ala 65	agi Se:	t gct r Ala	ggg Gly	g aa⊆ ⁄ Lys	g cac His 70	agg Arg	agt Ser	gag Glu	ato Ile	tcc Ser 75	gtg Val	g ato Met	aca Thi	a gct	acc Thr 80	241
	gta Val	gt. Va	c tto l Phe	c ato	ato Met	g gto Val	cct Pro	ttc Phe	tct Ser	atg Met	att : Ile	gto Val	acc L Thi	tct Sei	t tac r Ty: 95	c atc r Ile	289

cgc atc ctg ggt gcc atc cta gca atg act tcc acc cag agc cgc cac Arg Ile Leu Gly Ala Ile Leu Ala Met Thr Ser Thr Gln Ser Arg His 100 105 110

aag gtc ttc tcc acc tgc tcc tcc cat ctg ctt gtg gtc tgt ctc ttc 385 Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Cys Leu Phe 115 120 125
ttt gga aca gcc agc atc acc tac ata cgg ccc cag gca ggc tcc tct 433 Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser 130 140
gtc acc aca gac cgc atc ctc agt ctc ttc tac acg gtc atc aca ccc 481 Val Thr Thr Asp Arg Ile Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro 145 150 155 160
atg ctc Met Leu
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Ala Cys Met Thr Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr 20 25 30
Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Pro Ser His 35 40 45
Pro Met Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu 50 55 60
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr 65 70 75 80
Val Val Phe Ile Met Val Pro Phe Ser Met Ile Val Thr Ser Tyr Ile 85 90 95
Arg Ile Leu Gly Ala Ile Leu Ala Met Thr Ser Thr Gln Ser Arg His 100 105 110
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Cys Leu Phe 115 120 125

Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser 130 135 140

Val	Thr	Thr	Asp	Arg	Ile	Leu	Ser	Leu	Phe	Tyr	Thr	Val	Ile	Thr	Pro
145			_	_	150					155					160

Met Leu

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Val Cys Ala Leu Ile Leu Val Leu Cys Trp Val Leu Thr Asn Val Val
                                                                          97
             20
gcc ttg acc cac aca ctc ctc atg gct cga ctg tcc ttc tgt gtg act
                                                                          145
Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
                              40
ggg gaa att gct cac ttt ttc tgt gac atc act cct gtc ctg aag cta
                                                                          193
Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
    50
tca tgt tct gac acc cac atc aat gag atg atg gtt ttt gtc ttg gga
                                                                          241
Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
                                           75
ggc aca gta ctc atc atc ccc ttt cta tgc att gtc acc tcc tac atc
                                                                          289
Gly Thr Val Leu Ile Ile Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
                 85
tac att gtg cct gct att ctg agg gtc cga acc cat ggt ggg gcg ggc
                                                                          337
Tyr Ile Val Pro Ala Ile Leu Arg Val Arg Thr His Gly Gly Ala Gly
aag gcc ttt tcc acc tgc agt tcc cac ctc tgc att gtt tgt gtg ttc
                                                                          385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Val Phe
         115
                              120
tat ggg acc ctc ttc agt gcc tac ctg tgt cct ccc tcc atc gcc tct
                                                                          433
 Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
     130
 gaa gat aag gac att gca aca gct gca atg tat acc ata gtg act ccc
                                                                          481
 Glu Asp Lys Asp Ile Ala Thr Ala Ala Met Tyr Thr Ile Val Thr Pro
                                           155
                      150
 145
                                                                          487
 acg ttg
 Thr Leu
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Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
                     70
Gly Thr Val Leu Ile Ile Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
Tyr Ile Val Pro Ala Ile Leu Arg Val Arg Thr His Gly Gly Ala Gly
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Val Phe
Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
                         135
Glu Asp Lys Asp Ile Ala Thr Ala Ala Met Tyr Thr Ile Val Thr Pro
 Thr Leu
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Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
                                                                                49
gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg
Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
                                                                                97
                                                                               145
gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt tca gaa
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
aat ctt gtc aat cac tac atg tgt gat gtc ctt ccc ctc ctt gag ctc
                                                                               193
Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
     50
tee tge aac age tet tae ata aat ttg etg ttg gtt ttt att att gtg
                                                                               241
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val
                       70
gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
                                                                               289
ttt att ctt tcc agc att ctc cac att agc tcc aca gag ggc agg tct
                                                                               337
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
              100
aaa gcc ttc agt acc tgc agc tcc cac ata att gtg gta tcg ctt ttc
                                                                                385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
                                120
          115
ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc
                                                                                433
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
                            135
     130
ctg gac cag ggg aaa gtg tct tcc att ttt tat act gca gtg gtg cca
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Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
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Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val
Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
                85
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
                                105
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
                            120
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Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
Cys
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  Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly
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tac tgt gga cag ctg gtg gct ttc tct tac atg agt ggt ttc atg atc Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile

tct gtc atc aag gtc tat ttc att tca cat gtt gct ttc tgt ggc tcc Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser aat gtt atg aac ctc ttt ttc tgt gat atc tca cca gtc cta aaa ctg Asn Val Met Asn Leu Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu 55

25

gca tgc aaa gac atg tcc aca gct gag cta gtg gac ttt gct tta gct 241 Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala 70 -

145

193

atc gtc att ctt gtg atc cct ctc att acc act atc ctc tcc tat atc 289 Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile 85

tac att gtc tcc gcc att ctg cat ata ccc tcc acc cag gga agg aag 337 Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys 100 105

aag gcc ttc tcc acc tgt gca tct cac ctc act gta gtc ata att ttt 385 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe 120

tac aca gcc atg att ttt aca tat gtt cgg ccc aga gct att gca tca 433 Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser 140 135

ttt aat tcc aac aaa cta atc tca gct gtc tat gca gtc ctc aca ccc 481 Phe Asn Ser Asn Lys Leu Ile Ser Ala Val Tyr Ala Val Leu Thr Pro

487 atg cta Met Leu

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<211> 162

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Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile 20 25

Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser

Asn Val Met Asn Leu Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu

Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile 90 Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys 105 110 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser 130 135 Phe Asn Ser Asn Lys Leu Ile Ser Ala Val Tyr Ala Val Leu Thr Pro 145 Met Leu <210> 363 488 <211> DNA <212> <213> Saimiri boliviensis <220> <221> misc\_feature (1)..(488)<222> <223> Taxon = 27679; gene = SBO220; pseudogene; Accession DDBJ/EMBL/GenBank = AF179840 <400> 363 tgtggccatc tgtaagcccc tgcattacac caccatcatg agcagcaaaa tctgcctgca 60 gettgtgett gggtgetggg ttettggttt teteateate ttteeaceae teetettagg 120 actaaatett gaettetgtg eetecaaegt egttgateat ttetaetgtg acaetateee 180 gctcctgcag atttcctgca cagacacgca gctcctggag aggatgggat tcatctcagc 240 gctggtgaca ctcttagtca cattggtaat ggtgataata tcatatactt atattgccct 300 gacaattcta aaaatccctt caactagtca gaggaaaaag gctttttcca cgtgttcttc 360 tcacatgatt gtgatatccc tttcttatgg cagctgccat cttcatgtat gttaagccat 420 cagtcaaaca aagggtatct ttttcaaagg gaatttcggt gctcaatacc tctgttgctc 480 488 cacttttg

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 Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
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ctg tct cgc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat
Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
            20
gcc atg ttg cac act tta ctc ata gcc agg ttg cgt ttt tgt gca gac
                                                                      145
Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp
                            40
                                                                      193
aat gtg atc ttc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg
Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
gcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga
                                                                      241
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
                    70
ggc ctc att ctt gtc atc cca ttt cta ctt atc att ggg tcc tac gca
                                                                      289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
cga att gtc ttc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc
                                                                      337
Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
            100
                                105
aag gcc gtc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc
                                                                      385
Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
        115
tat ggg act gtt att ggt ctc tac tta tgc cca tca gct aat aat tct
                                                                       433
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
                         135
act cta aag gag act gtc atg gct gtg atg tac act gtg atg gcc ccc
                                                                       481
Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
                                         155
                     150
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atg ctg
Met Leu
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Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
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Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His

Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp

Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly 70

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala

Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys

Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser 135 130

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Met Leu

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gtg tgt ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg

97

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Val	Cys	Leu	Leu 20	Leu	Leu	Leu	Gly	Val 25	Tyr	Gly	Met	Gly	Val 30	Leu	Gly		
gct Ala	gtg Val	gct Ala 35	cat His	aca Thr	gga Gly	aat Asn	ata Ile 40	gtg Val	ttt Phe	cta Leu	acc Thr	ttt Phe 45	tgt Cys	gca Ala	ggc Gly	145	
aac Asn	ctt Leu 50	gtc Val	aat Asn	cac His	tac Tyr	atg Met 55	tgt Cys	gac Asp	atc Ile	ctt Leu	ccc Pro 60	ctt Leu	ctt Leu	gag Glu	ctc Leu	193	
tcc Ser 65	tgc Cys	aat Asn	ggc Gly	tct Ser	tac Tyr 70	ata Ile	aat Asn	gtt Val	ctg Leu	gtc Val 75	atc Ile	ttt Phe	att Ile	gtt Val	gtg Val 80	241	
acc Thr	att Ile	ggc Gly	att Ile	999 Gly 85	gtg Val	ccc Pro	att Ile	gtt Val	gcc Ala 90	att Ile	ttt Phe	atc Ile	tct Ser	tat Tyr 95	ggt Gly	289	
ttt Phe	att Ile	ctt Leu	tcc Ser 100	agc Ser	aat Asn	ctc Leu	cac His	att Ile 105	agt Ser	tct Ser	gct Ala	gag Glu	ggc Gly 110	agg Arg	tct Ser	337	
aaa Lys	gcc Ala	ttc Phe 115	agt Ser	acc Thr	tgc Cys	agc Ser	tcc Ser 120	cac His	ata Ile	att Ile	gca Ala	gtt Val 125	tct Ser	ctt Leu	ttc Phe	385	
ttc Phe	ggg Gly 130	Ser	gga Gly	gct Ala	ttt Phe	atg Met 135	Tyr	ctc Leu	aaa Lys	ccc Pro	tct Ser 140	tcc Ser	gtt Val	tta Leu	ccc Pro	433	
ctg Leu 145	Asp	cag Gln	ggg	aaa Lys	gta Val 150	Ser	tcc Ser	ctg Leu	ttt Phe	tat Tyr 155	Thr	att Ile	gtg Val	gtg Val	CCC Pro 160	481	
_	ttt Phe															487	
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Va: 1	l Ala	a Ile	э Суя	s Asr 5	n Pro	) Let	ı Leı	а Туз	Met 10	: Val	L Thi	. Met	: Sei	15	Gln		
Va:	l Cy:	s Lei	ı Lei 20	ı Leı	ı Lei	ı Leı	ı Gly	y Va: 25	l Ty:	r Gly	y Met	: Gly	y Va: 30	l Le	ı Gly		
Al	a Vai	1 Ala 35	a Hi	s Th	r Gl	y Ası	n Ile 40	e Va	l Ph	e Lei	ı Thi	r Phe 45	е Су	s Ala	a Gly		
As	n Le	u Va	l As	n Hi	в Ту	r Me 55	t Cy	s As	p Il	e Le	u Pro 60	o Le	u Le	u Gl	u Leu		

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Ser Cys Asn Gly Ser Tyr Ile Asn Val Leu Val Ile Phe Ile Val Val
                     70
Thr Ile Gly Ile Gly Val Pro Ile Val Ala Ile Phe Ile Ser Tyr Gly
Phe Ile Leu Ser Ser Asn Leu His Ile Ser Ser Ala Glu Gly Arg Ser
                                 105
            100
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe
                             120
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Ser Ser Val Leu Pro
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Met Phe
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                                                                           97
ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
             20
                                  25
tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac
                                                                          145
Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
         35
                              40
                                                                          193
ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc ata cat ctt
Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
gcc tgt tat gac act ttc ctt aat gat gtg gtg atg tat ttg gca gct Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
                                                                          241
                                           75
                      70
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atg ctg ctg ggc ggt ggt ccc ctc aca gga att att tac tct tac tct Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser 85 90 95	289
aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag tac Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr 100 105 110	337
aag gcg ttt tcc acc tgt gca tct cac atc tta att gtc tcc tta ttt Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe 115 120 125	385
tat ggt aca ctc cta ggt gtg tac ctt agt tct gct gca act ggc aac Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 130 135 140	433
tca cat tca agt gct gca gcc ttg gtg atg tac act gtg gtc acc ccc Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro 145 150 160	481
atg ctg Met Leu	487
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Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe



Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 130 135 140

Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

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act Thr	atc Ile	cac His	aca Thr 20	cag Gln	agc Ser	aaa Lys	ttc Phe	atc Ile 25	tct Ser	ttc Phe	tcg Ser	ggc Gly	tgc Cys 30	atc Ile	aca Thr	97
cag Gln	ata Ile	ttt Phe 35	ttc Phe	ttc Phe	att Ile	gtg Val	ttt Phe 40	gga Gly	tgc Cys	ctg Leu	gac Asp	aat Asn 45	tta Leu	ctc Leu	cta Leu	145
tca Ser	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgc Cys 60	cat His	ccc Pro	ttg Leu	cac His	193
tat Tyr 65	gtg Val	gtc Val	atc Ile	atg Met	aat Asn 70	tct Ser	tgc Cys	ttc Phe	tgt Cys	gtg Val 75	atg Met	ctg Leu	gct Ala	ctt Leu	gga Gly 80	241
tca Ser	tgg Trp	ata Ile	gtc Val	agc Ser 85	gtc Val	atg Met	agt Ser	tcc Ser	cta Leu 90	cct Pro	gag Glu	acc Thr	ttg Leu	act Thr 95	gtg Val	289
tta Leu	aga Arg	cta Leu	tcc Ser 100	ttc Phe	tgt Cys	aca Thr	aac Asn	atg Met 105	gaa Glu	att Ile	cca Pro	cac His	ttt Phe 110	ttc Phe	tgt Cys	337
gat Asp	ctt Leu	ccc Pro 115	gaa Glu	gtc Val	ctg Leu	aag Lys	ctt Leu 120	Ala	tgt Cys	tct Ser	gac Asp	acc Thr 125	ctt Leu	gtt Val	aat Asn	385

aac att gtg aca tat tct ata acc ata gtc ata gct ggt ttc cca ttc



Asn Ile Val Thr Tyr Ser Ile Thr Ile Val Ile Ala Gly Phe Pro Phe 130 135 140	
tct ggg att cta ttg tct tat tct aag att ttc tcc tcc atc cta aga Ser Gly Ile Leu Leu Ser Tyr Ser Lys Ile Phe Ser Ser Ile Leu Arg 145 150 155 160	481
att cct tca gct ggg ggc aag tac aaa gcc ttt tct acc tgt ggg tct Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175	529
cat ctt ttg gtg gtc ttc tta ttc tat agc aat ggt ctt ggg gtc tac His Leu Leu Val Val Phe Leu Phe Tyr Ser Asn Gly Leu Gly Val Tyr 180 185 190	577
ctc agc tct gca gcc aca tca tct tct aga atg agt cta gtt gcc tca Leu Ser Ser Ala Ala Thr Ser Ser Ser Arg Met Ser Leu Val Ala Ser 195 200 205	625
ctg atg tac agc ata gtc act ccc Leu Met Tyr Ser Ile Val Thr Pro 210 215	649
<210> 371 <211> 216 <212> PRT	
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115 120 125

Asn	Ile 130	Val	Thr	Tyr	Ser	11e 135	Thr	IIe	Val	11e	140	GIÀ	Pne	Pro	Pne	
Ser 145	Gly	Ile	Leu	Leu	Ser 150	Tyr	Ser	Lys	Ile	Phe 155	Ser	Ser	Ile	Leu	Arg 160	
Ile	Pro	Ser	Ala	Gly 165	Gly	Lys	Tyr	Lys	Ala 170	Phe	Ser	Thr	Сув	Gly 175	Ser	
His	Leu	Leu	Val 180	Val	Phe	Leu	Phe	Tyr 185	Ser	Asn	Gly	Leu	Gly 190	Val	Tyr	
Leu	Ser	Ser 195	Ala	Ala	Thr	Ser	Ser 200	Ser	Arg	Met	Ser	Leu 205	Val	Ala	Ser	
Leu	Met 210	Tyr	Ser	Ile	Val	Thr 215	Pro									
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aac Asn	atg Met	caa Gln	agc Ser 20	caa Gln	gtt Val	cca Pro	tcc Ser	ata Ile 25	ccc	tat Tyr	gca Ala	ggt Gly	tgc Cys 30	ctg Leu	gca Ala	97
caa Gln	atg Met	tac Tyr 35	ttt Phe	ttc Phe	ctg Leu	ctt Leu	ttt Phe 40	gca Ala	gat Asp	ctc Leu	gag Glu	agc Ser 45	ttc Phe	ctc Leu	ctt Leu	145
gtg Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gat Asp	cgc Arg 55	tat Tyr	gtg Val	gcc Ala	ato Ile	tgc Cys 60	ttc Phe	ccc Pro	cta Leu	cac His	193
tat Tyr	act Thr	ago Ser	ato Ile	atg Met	ago Ser	ccc	aag Lys	ctg Leu	tgt Cys	ctc Leu 75	tgc Cys	ctg Leu	gtg Val	gca Ala	cta Leu 80	241

289

tct tgg cta ctg acc aca gtc atc tct ttg tca cac aca ctg ctc atg

Ser	Trp	Leu	Leu	Thr 85	Thr	Val	Ile	Ser	Leu 90	Ser	His	Thr	Leu	Leu 95	Met	
gct Ala	cgg Arg	ctc Leu	tcc Ser 100	ttc Phe	tgt Cys	gct Ala	aac Asn	aat Asn 105	gtg Val	att Ile	cct Pro	cac His	ttt Phe 110	ttc Phe	tgt Cys	337
gat Asp	atg Met	tca Ser 115	gct Ala	ctt Leu	ctg Leu	aag Lys	tta Leu 120	gcc Ala	tgc Cys	tct Ser	gac Asp	att Ile 125	cag Gln	atc Ile	aat Asn	385
aag Lys	ttg Leu 130	atg Met	ata Ile	ttt Phe	atc Ile	ttg Leu 135	gga Gly	gga Gly	ctt Leu	gtc Val	att Ile 140	att Ile	gtc Val	cca Pro	ttc Phe	433
ctg Leu 145	ctg Leu	ata Ile	ttt Phe	tca Ser	tcc Ser 150	tat Tyr	gca Ala	cga Arg	ata Ile	gtg Val 155	tcc Ser	tcc Ser	att Ile	ctc Leu	aag Lys 160	481
gtc Val	ccc Pro	tct Ser	tct Ser	aga Arg 165	agc Ser	atc Ile	cgc Arg	aag Lys	gcc Ala 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	ggt Gly 175	tcc Ser	529
cac His	ctc Leu	tct Ser	gtg Val 180	gtg Val	tct Ser	ctt Leu	ttc Phe	tat Tyr 185	Gly 999	aca Thr	atc Ile	att Ile	ggt Gly 190	ctc Leu	tat Tyr	577
tta Leu	cgt Arg	cca Pro 195	tca Ser	gct Ala	aat Asn	aat Asn	tca Ser 200	acc Thr	att Ile	aag Lys	gag Glu	act Thr 205	gtc Val	atg Met	gct Ala	625
gtg Val	atg Met 210	tac Tyr	acg Thr	gtg Val	gtg Val	acc Thr 215	cct Pro									649
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<40	0>	373														
Phe 1	Ser	Asp	Phe	Cys 5	Phe	Ser	Ser	Val	Thr 10	Ile	Pro	Lys	Leu	Leu 15	Gln	
Asn	Met	Gln	Ser 20	Gln	Val	Pro	Ser	11e 25	Pro	Tyr	Ala	Gly	Cys	Leu	Ala	
Glr	n Met	Tyr 35	Phe	Phe	. Leu	Leu	Phe 40	. Ala	Asp	Leu	. Glu	Ser 45	Phe	. Lev	Leu	
Va]	. Ala	. Met	Ala	туг	Asp	Arg 55	Туг	· Val	. Ala	ı Ile	е Сув 60	Ph∈	Pro	Leu	ı His	
Туз	Thr	s Ser	: Ile	e Met	: Ser	Pro	Lys	. Let	ı Cys	Lei	і Суя	s Lev	ı Val	Ala	a Leu	

75

Ser	Trp	Leu	Leu	Thr	Thr	Val	Ile	Ser	Leu	Ser	His	Thr	Leu	Leu	Met
	-			85					90					95	

Ala Arg Leu Ser Phe Cys Ala Asn Asn Val Ile Pro His Phe Phe Cys

Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Gln Ile Asn

Lys Leu Met Ile Phe Ile Leu Gly Gly Leu Val Ile Ile Val Pro Phe 130

Leu Leu Ile Phe Ser Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 150

Val Pro Ser Ser Arg Ser Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr

Leu Arg Pro Ser Ala Asn Asn Ser Thr Ile Lys Glu Thr Val Met Ala 205

Val Met Tyr Thr Val Val Thr Pro

<210> 374

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc\_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR10M; Accession DDBJ/EMBL/GenBank = AF073961

<220>

<221> CDS

<222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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97 aac atg cag agc cag gac tca tcc atc acc tat gca gga tgc ctg aca Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr 25

caa atg tac ttt ttc ttg ctc ttt gga gac ctt gag agc ttc ctc ctt 145 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu

35 40 45

gtg Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	ccc Pro	ctt Leu	cat His	193
tac Tyr 65	atg Met	agc Ser	atc Ile	atg Met	agc Ser 70	ccc Pro	agc Ser	ctc Leu	tgt Cys	gtg Val 75	agt Ser	ctg Leu	gtg Val	ctg Leu	ctg Leu 80	241
tcc Ser	tgg Trp	gtg Val	ctg Leu	acc Thr 85	act Thr	ttc Phe	cat His	gcc Ala	atg Met 90	ctg Leu	cat His	acc Thr	ctg Leu	ctc Leu 95	atg Met	289
gcc Ala	aga Arg	ttg Leu	tca Ser 100	ttc Phe	tgt Cys	gag Glu	gac Asp	aat Asn 105	gtg Val	atc Ile	ccc Pro	cac His	ttt Phe 110	ttc Phe	tgt Cys	337
gac Asp	atg Met	tct Ser 115	gct Ala	ctg Leu	ctg Leu	aag Lys	ctg Leu 120	tcc Ser	tgc Cys	tct Ser	gac Asp	act Thr 125	cac His	gtt Val	aat Asn	385
gaa Glu	ttg Leu 130	gtg Val	ata Ile	ttt Phe	gtc Val	aca Thr 135	gga Gly	ggc Gly	ctg Leu	atc Ile	ctt Leu 140	gtc Val	att Ile	cca Pro	ttt Phe	433
gtg Val 145	ctc Leu	atc Ile	ctt Leu	gtg Val	tcc Ser 150	tat Tyr	gca Ala	cga Arg	att Ile	gtg Val 155	tcc Ser	tcc Ser	att Ile	ctc Leu	aag Lys 160	481
gtc Val	ccg Pro	tct Ser	gct Ala	cga Arg 165	ggc Gly	atc Ile	cgt Arg	aaa Lys	gcc Ala 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	999 Gly 175	tcc Ser	529
cac His	ctg Leu	tct Ser	gtg Val 180	Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	GГУ	gca Ala	atc Ile	att Ile	ggt Gly 190	ьeu	tac Tyr	577
tta Leu	tgt Cys	cca Pro 195	Ser	gct Ala	gat Asp	aac Asn	tct Ser 200	Thr	gtg Val	aag Lys	gaa Glu	act Thr 205	gtc Val	atg Met	gcc Ala	625
atg Met	atg Met 210	Tyr	aca Thr	gtg Val	gtg Val	act Thr 215	ccc Pro									649
<21 <21 <21 <21	1>	375 216 PRT Mus	musc	ulus	dom	nesti	cus									
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<40	00>	375														
Phe 1	e Sei	Asp	) Let	ı Cys 5	s Phe	e Ser	Ser	Val	1 Thi	. Met	: Pro	Lys	s Leu	ı Let 15	ı Gln	

Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr 20 25 30

Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55

Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys

Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn

Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe

Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 150

Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 165

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr

Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala 200

Met Met Tyr Thr Val Val Thr Pro 210

<210> 376

<211> 649

<212> DNA <213> Mus musculus domesticus

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<221> misc\_feature

(1)..(649)

<223> Taxon = 10092; clone = OR11M; Accession DDBJ/EMBL/GenBank = AF073962

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 376

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aat atg cag agc cag gac cca tcc atc ccc tat gga ggt tgc ctg gca Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Gly Gly Cys Leu Ala 20 25 30	97
caa ata ttc ttc ttt atg ctt ttt gga gac atg gaa agc ttc ctt ctt Gln Ile Phe Phe Phe Met Leu Phe Gly Asp Met Glu Ser Phe Leu Leu 35 40 45	145
gta gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctg cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60	193
tac act agc atc atg agt cct aag gtc tgt act ttt cta gtg cta ctg Tyr Thr Ser Ile Met Ser Pro Lys Val Cys Thr Phe Leu Val Leu Leu 65 70 75 80	241
ttg tgg ata ctg aca aca cca cat gcc aca atg caa att ctg ctc aca Leu Trp Ile Leu Thr Thr Pro His Ala Thr Met Gln Ile Leu Leu Thr 85 90 95	289
gta aga ctg tct ttt tgt gag aac aat gtg ttt ctc aac ttt ttc tgt Val Arg Leu Ser Phe Cys Glu Asn Asn Val Phe Leu Asn Phe Phe Cys 100 105 110	337
gac ata ttt gtt ctc tta aag ctg gcc tgc tca gac act tat gtt aat Asp Ile Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 115 120 125	385
gat ttg atg ata ctt atc atg gga ggg ctc atc att gtt att cca ttc Asp Leu Met Ile Leu Ile Met Gly Gly Leu Ile Ile Val Ile Pro Phe 130 135 140	433
ctg ctc att gtt ata tcc tat gca agg atc atc tcc tct act ctt aag Leu Leu Ile Val Ile Ser Tyr Ala Arg Ile Ile Ser Ser Thr Leu Lys 145 150 150	481
gtt cca tct act caa ggc atc cac aag gtc ttc tct acc tgt ggc tct Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175	529
cat ctg tct gtg gtg tct ctg ttc tat ggg aca att att ggt ctc tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	577
tta tgt cca tca ggt aat aat ttc agt cta aag ggg tct gcc atg gct Leu Cys Pro Ser Gly Asn Asn Phe Ser Leu Lys Gly Ser Ala Met Ala 195 200 205	625
atg atg tac aca gtg gtg act ccc Met Met Tyr Thr Val Val Thr Pro 210 215	649
<210> 377 <211> 216 <212> PRT <213> Mus musculus domesticus	
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Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln

Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Gly Gly Cys Leu Ala

Gln Ile Phe Phe Phe Met Leu Phe Gly Asp Met Glu Ser Phe Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50

Tyr Thr Ser Ile Met Ser Pro Lys Val Cys Thr Phe Leu Val Leu Leu

Leu Trp Ile Leu Thr Thr Pro His Ala Thr Met Gln Ile Leu Leu Thr

Val Arg Leu Ser Phe Cys Glu Asn Asn Val Phe Leu Asn Phe Phe Cys

Asp Ile Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 125

Asp Leu Met Ile Leu Ile Met Gly Gly Leu Ile Ile Val Ile Pro Phe 130

Leu Leu Ile Val Ile Ser Tyr Ala Arg Ile Ile Ser Ser Thr Leu Lys 145

Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr

Leu Cys Pro Ser Gly Asn Asn Phe Ser Leu Lys Gly Ser Ala Met Ala 200 195

Met Met Tyr Thr Val Val Thr Pro 215

<210> 378

<211> 649 <212> DNA

<213> Mus musculus domesticus

<220>

<221> misc\_feature

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<222 <223	L > ( 2 >	(2). Produ	-	-	facto	ory 1	recep	ptor	; re	gion	betv	ween	traı	nsmer	mbrane	domain	s
	c to									ar Me					ta cag eu Gln	49	
												ggc Gly				97	
	_				_	_			_	_		agc Ser 45				145	
												ttc Phe				193	
												ctg Leu				241	
												act Thr				289	
tct Ser	aga Arg	ttg Leu	tca Ser 100	ttc Phe	tgt Cys	gag Glu	gat Asp	aac Asn 105	ttg Leu	atc Ile	cac His	cac His	ttt Phe 110	ttc Phe	tgt Cys	337	
gac Asp	ata Ile	tct Ser 115	gcc Ala	ctg Leu	ctc Leu	aag Lys	ttg Leu 120	gct Ala	tgc Cys	tct Ser	gac Asp	att Ile 125	cat His	att Ile	aat Asn	385	
gaa Glu	tta Leu 130	atg Met	ata Ile	ttt Phe	atc Ile	atg Met 135	gga Gly	999 Gly	ctt Leu	gtt Val	agc Ser 140	atc Ile	atc Ile	cca Pro	ttc Phe	433	
tta Leu 145	ctc Leu	att Ile	gtt Val	gtg Val	tcc Ser 150	tat Tyr	ata Ile	caa Gln	att Ile	gtc Val 155	tac Tyr	tcc Ser	att Ile	cta Leu	aag Lys 160	481	
												acc Thr				529	
												ttt Phe				577	
												att Ile 205			gcc Ala	625	
_	_	_			gtg Val											649	1

- <210> 379
- <211> 216
- <212> PRT
- <213> Mus musculus domesticus
- <220>
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- <222> (1)..(649)
- <223> Taxon = 10092; clone = OR12M; Accession DDBJ/EMBL/GenBank = AF073963
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- Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
  1 5 10 15
- Asn Met Gln Ser Gln Asp Thr Ser Ile Ser Tyr Ala Gly Cys Leu Thr 20 25 30
- Gln Met Tyr Phe Leu Leu Val Phe Gly Asp Leu Glu Ser Ile Leu Leu 35 40 45
- Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Phe Pro Leu His 50 60
- Tyr Met Ser Ile Met Ser Pro Thr Leu Cys Val Cys Leu Leu Val Leu 65 70 75 80
- Ser Trp Val Phe Thr Val Leu Tyr Ser Met Leu His Thr Leu Leu Leu 85 90 95
- Ser Arg Leu Ser Phe Cys Glu Asp Asn Leu Ile His His Phe Phe Cys
- Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
- Glu Leu Met Ile Phe Ile Met Gly Gly Leu Val Ser Ile Ile Pro Phe 130 135 140
- Leu Leu Ile Val Val Ser Tyr Ile Gln Ile Val Tyr Ser Ile Leu Lys 145 150 155 160
- Ile Ser Ser Ala His Val Leu His Lys Ile Phe Ser Thr Cys Gly Ser 165 170 175
- His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Phe Ala Leu Tyr 180 185 190
- Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Ile Ser Met Ala 195 200 205
- Met Met Cys Thr Val Val Thr Pro

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<210> 380
<211> 649
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<221>
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<223> Product = olfactory receptor; region between transmembrane domains
TM2 and TM7
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  Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Ile Pro Lys Met Leu Val
aat atc caa aca cag agc aag tcc atc tcc tat gca gaa tgc atc acc
                                                                          97
Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr Ala Glu Cys Ile Thr
                                  25
            20
                                                                         145
cag att tat ttt ttc atg ctc ttt gga ggc atg gac ata ctt ctc ctc
Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met Asp Ile Leu Leu
acc gtg atg gcc tat gac cga ttt gtg gcc atc tgt cac ccc ctt cac
                                                                         193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
                                                                         241
tat tca gtc att atg aat ccc caa cta agt ggc ttg ctg gtt ctt gta
Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly Leu Leu Val Leu Val
                                           75
tca tgg ttt att agc ttt tca tat tct ctg ata cag agt cta ttg atg
                                                                          289
Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
                 85
ctg cgg ttg tcc ttc tgt aca aat cag ata att aaa cac ttt tac tgt
Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile Lys His Phe Tyr Cys
                                                                          337
                                  105
             100
                                                                          385
gaa tat tot aga goo oto act ata goo tgo toa gao aca ota ato aat
Glu Tyr Ser Arg Ala Leu Thr Ile Ala Cys Ser Asp Thr Leu Ile Asn
                              120
cat atc ctt ctt tat att ctg ata tgt gtc ctt ggc ttc atc cct ttc
                                                                          433
His Ile Leu Leu Tyr Ile Leu Ile Cys Val Leu Gly Phe Ile Pro Phe
                          135
                                               140
                                                                          481
tca ggg atc ctt tat tca tac tgt aaa att gtt tct tct att ttg aga
Ser Gly Ile Leu Tyr Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg
                                           155
                                                                          529
att cca tca aca gat gga aaa tat aaa gca ttt tct acc tgt ggg tct
Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
                 165
                                                                          577
cat cta tca gtg gtt tct tta ttc tat ggg aca ggc ctt ggt gtg tac
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His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
            180
                                  185
ctt agt tct gat gta act tcc tcc tct ggg aag gac gtg gtg gcc tca
Leu Ser Ser Asp Val Thr Ser Ser Ser Gly Lys Asp Val Val Ala Ser
                                                                           625
                              200
                                                    205
                                                                           649
gta atg tat aca gtg gtc acc cct
Val Met Tyr Thr Val Val Thr Pro
    210
<210> 381
<211> 216
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<213> Mus musculus domesticus
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AF073964
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Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr Ala Glu Cys Ile Thr
Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met Asp Ile Leu Leu
                              40
         35
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly Leu Leu Val Leu Val
Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
                                       90
Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile Lys His Phe Tyr Cys
                                                         110
Glu Tyr Ser Arg Ala Leu Thr Ile Ala Cys Ser Asp Thr Leu Ile Asn
                               120
         115
His Ile Leu Leu Tyr Ile Leu Ile Cys Val Leu Gly Phe Ile Pro Phe
 Ser Gly Ile Leu Tyr Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg
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Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser

150

145

155

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr

Leu Ser Ser Asp Val Thr Ser Ser Ser Gly Lys Asp Val Val Ala Ser 200

Val Met Tyr Thr Val Val Thr Pro

<210> 382

<211> 643

<212> DNA <213> Mus musculus domesticus

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<222> (2)..(643) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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gac ctc cta tcg gcg aag aaa acc atc tca ata gaa ggc tgc ctg gct Asp Leu Leu Ser Ala Lys Lys Thr Ile Ser Ile Glu Gly Cys Leu Ala 20

cag gtc ttt ttt gtg ttt ttt cct tct ggt act gaa gcc tgc ctg ctc 145 Gln Val Phe Phe Val Phe Phe Pro Ser Gly Thr Glu Ala Cys Leu Leu 40 35

tet gte atg get tat gac ege tat get gee ate tge eat eee etg ete 193 Ser Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Leu 55 50

tac ggc cag gtg atg aga aat gag ttg tgt gta agg ctt gtg gtc atc 241 Tyr Gly Gln Val Met Arg Asn Glu Leu Cys Val Arg Leu Val Val Ile

289 tca tgg ggc gtg gcc tct ctc aac gca acc atc atc gtg ctc ttg gct Ser Trp Gly Val Ala Ser Leu Asn Ala Thr Ile Ile Val Leu Leu Ala 90

gtc aac ctg gac ttc tgt ggg gct caa acc att cac cac tac acc tgt 337 Val Asn Leu Asp Phe Cys Gly Ala Gln Thr Ile His His Tyr Thr Cys 100

gag ctg cct gcc ctt ttc ccc ttg tcc tgt tcc gat atc tcc atc act 385 Glu Leu Pro Ala Leu Phe Pro Leu Ser Cys Ser Asp Ile Ser Ile Thr 120 115

gtc gtc gtc ctg ctt tgc tcc agc ttg ctg cat ggg ctg gga acc ttt 433

Val Val Va	al Leu	Leu (		Ser 135	Ser	Leu	Leu	His	Gly 140	Leu	Gly	Thr	Phe	
atc cct at Ile Pro I	tc ttc le Phe	Phe :	tcc ' Ser '	tat	gcc Ala	cgc Arg	att Ile	Val	tcc	gcc Ala	atc Ile	ttg Leu	agc Ser 160	481
atc agt to	cc acc er Thr	acc	150 ggg : Gly :	agg Arg	agc Ser	aag Lys	Ala	ttc Phe	tcc Ser	acc Thr	tgc Cys	Ser	tcc	529
cac ctc g	at aca	165	a.c.c	t t a	ttc	+++	170	tet	aac	ttt	ctt	175	tat	577
His Leu A	la Ala 180	Val	Thr	Leu	Phe	Phe 185	Gly	Ser	Gly	Phe	Leu 190	Cys	Tyr	
ctc atg c Leu Met P 1	cg cct ro Pro 95	tct Ser	ggt Gly	tct Ser	tct Ser 200	ctg Leu	gac Asp	ttg Leu	ctc Leu	ttg Leu 205	tcg Ser	ttg Leu	cag Gln	625
tac agc g Tyr Ser A 210														643
<210> 38 <211> 21 <212> PR <213> Mu	.4	ılus	dome	stic	cus									
<220> <221> mi	sc feat	ture												
Z2225 (1	) (64	3)												
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<223> Ta AF073965 <400> 38	axon = 1	10092												k =
<223> Ta AF073965	axon = 1	10092												k =
<223> Ta AF073965 <400> 38	axon = 1 33 Asp Leu	0092 Cys 5	Phe	Ser	Ser	Val	Thr 10	Val	Pro	Lys	Leu	Leu 15	Lys	k =
<pre>&lt;223&gt; Ta AF073965 &lt;400&gt; 38 Phe Val A 1 Asp Leu I Gln Val B</pre>	axon = 33 Asp Leu Leu Ser 20	Cys 5 Ala Val	Phe Lys	Ser Lys Phe	Ser Thr Pro	Val Ile 25	Thr 10 Ser	Val Ile	Pro Glu Glu	Lys Gly	Leu Cys 30	Leu 15 Leu	Lys Ala	k =
<pre>&lt;223&gt; Ta AF073965 &lt;400&gt; 38 Phe Val A 1 Asp Leu I Gln Val B</pre>	axon = 1 33 Asp Leu Leu Ser 20 Phe Phe	Cys 5 Ala Val	Phe Lys Phe	Ser Lys Phe	Ser Thr Pro	Val Ile 25 Ser	Thr 10 Ser	Val Ile Thr	Pro Glu Glu	Lys Gly Ala 45	Leu Cys 30	Leu 15 Leu Leu	Lys Ala Leu	k =
<pre>&lt;223&gt; Ta AF073965 &lt;400&gt; 38 Phe Val A 1  Asp Leu I  Gln Val I 3</pre>	Asp Leu Leu Ser 20 Phe Phe 35	Cys 5 Ala Val	Phe Lys Phe Asp	Ser Lys Phe Arg	Ser Thr Pro 40	Val Ile 25 Ser	Thr 10 Ser Gly	Val Ile Thr	Pro Glu Glu Cys	Lys Gly Ala 45	Leu Cys 30 Cys	Leu 15 Leu Leu	Lys Ala Leu Leu	k =
<pre>&lt;223&gt; Ta AF073965 &lt;400&gt; 38 Phe Val A 1  Asp Leu I  Gln Val I  Ser Val N 50</pre>	axon =  33  Asp Leu  Leu Ser 20  Phe Phe 35  Met Ala  Gln Val	Cys 5 Ala Val Tyr	Phe Lys Phe Asp	Ser Lys Phe Arg 55	Ser Thr Pro 40 Tyr	Val Ile 25 Ser Ala	Thr 10 Ser Gly Ala	Val Ile Thr Ile Val 75	Pro Glu Glu Cys 60	Lys Gly Ala 45 His	Cys 30 Cys Pro	Leu 15 Leu Leu Val	Lys Ala Leu Leu Ile 80	k =
<pre>&lt;223&gt; Ta AF073965 &lt;400&gt; 38 Phe Val A 1  Asp Leu I  Gln Val I  Ser Val N 50  Tyr Gly 0 65</pre>	Asp Leu Leu Ser 20 Phe Phe 35 Met Ala Gln Val	Cys 5 Ala Val Tyr Met Ala 85	Phe Lys Phe Asp Arg 70 Ser	Ser Lys Phe Arg 55 Asn	Ser Thr Pro 40 Tyr Glu	Val Ile 25 Ser Ala	Thr 10 Ser Gly Ala Cys	Val Thr Ile Val 75	Pro Glu Glu Cys 60 Arg	Lys Gly Ala 45 His	Leu Cys 30 Cys Pro Val	Leu Leu Val Leu 95	Lys Ala Leu Leu Ile 80 Ala	k =

115 120 125

Val	Val 130	Val	Leu	Leu	Суѕ	Ser 135	Ser	Leu	Leu	His	Gly 140	Leu	Gly	Thr	Phe	
Ile 145	Pro	Ile	Phe	Phe	Ser 150	Tyr	Ala	Arg	Ile	Val 155	Ser	Ala	Ile	Leu	Ser 160	
Ile	Ser	Ser	Thr	Thr 165	Gly	Arg	Ser	Lys	Ala 170	Phe	Ser	Thr	Cys	Ser 175	Ser	
His	Leu	Ala	Ala 180	Val	Thr	Leu	Phe	Phe 185	Gly	Ser	Gly	Phe	Leu 190	Cys	Tyr	
Leu	Met	Pro 195	Pro	Ser	Gly	Ser	Ser 200	Leu	Asp	Leu	Leu	Leu 205	Ser	Leu	Gln	
Tyr	Ser 210	Ala	Val	Thr	Pro											
<210 <211 <212 <213	L> 6 2> I	884 543 ONA Mus r	nusci	ulus	dome	estio	cus									
<220 <220 <220 <220 AF0	L> 1		(64)	3)	2; c.	lone	= O	R15-	71M2	1; A	cces	sion	DDB	J/EM	BL/GenE	Bank =
<221 <221 <221 <221 TM2	1> (		.(64 uct	3) = ol	facto	ory:	rece	ptor	; re	gion	bet	ween	tra	nsme	mbrane	domains
<40 C C L	tt a	384 tt ga al A	ac a sp I	tc t le P	tc t he P	tc t he S	cc t er S	ct g er V	ta a al T 1	hr I	tt c	cc a ro L	ag a ys M	et L	tg gcc eu Ala 5	49
aac Asn	cat His	ctc Leu	cta Leu 20	ggt Gly	agc Ser	aag Lys	gcc Ala	atc Ile 25	tcc Ser	ttt Phe	ggg ggg	gga Gly	tgt Cys 30	atg Met	gca Ala	97
cag Gln	atg Met	tac Tyr 35	ttc Phe	atg Met	ata Ile	tca Ser	ttg Leu 40	gga Gly	aac Asn	aca Thr	gac Asp	agt Ser 45	tat Tyr	ata Ile	cta Leu	145
gct Ala	gca Ala 50	atg Met	gca Ala	tat Tyr	gac Asp	cga Arg 55	gct Ala	gtg Val	gct Ala	atc Ile	agt Ser 60	cgc Arg	ccg Pro	ctt Leu	cat His	193
tat Tyr 65	gca Ala	aca Thr	att Ile	atg Met	agt Ser 70	cca Pro	caa Gln	ctt Leu	tgt Cys	gtc Val 75	ctg Leu	ctg Leu	gtt Val	gct Ala	80 GlA G33	241
							225	g g a	ata			200	cta	ctc	aca	289

Ser Trp Va	al Ile	Ala 85	Asn	Ala	Asn	Ala	Leu 90	Pro	His	Thr	Leu	Leu 95	Thr	
gct aga ti Ala Arg Le	g tcc eu Ser 100	ttc Phe	tgt Cys	ggc Gly	aat Asn	aag Lys 105	gat Asp	gtg Val	gcc Ala	aac Asn	ttc Phe 110	tac Tyr	tgt Cys	337
gac att ac Asp Ile Th	ca cct nr Pro 15	ttg Leu	ctc Leu	cag Gln	ctg Leu 120	tcc Ser	tgt Cys	tct Ser	gac Asp	atc Ile 125	cgc Arg	ttc Phe	aat Asn	385
gtg aag at Val Lys Me 130	g atg et Met	tac Tyr	ctt Leu	999 Gly 135	gtg Val	Gly aaa	gtc Val	ttc Phe	tct Ser 140	gtg Val	cca Pro	ctg Leu	ctg Leu	433
tgc atc at Cys Ile II 145	cc atc le Ile	tcc Ser	tat Tyr 150	gtc Val	cgg Arg	gtc Val	ttt Phe	tcc Ser 155	aca Thr	gtc Val	ttg Leu	cgg Arg	gtt Val 160	481
cca tct a Pro Ser T	cc aag hr Lys	ggc Gly 165	ttc Phe	ctg Leu	aag Lys	gcc Ala	ttg Leu 170	tcc Ser	acc Thr	tgt Cys	ggc Gly	tct Ser 175	cac His	529
ctg aca g Leu Thr V	tg gtg al Val 180	Ser	ttg Leu	tat Tyr	tat Tyr	999 Gly 185	aca Thr	gtc Val	atg Met	ggc Gly	atg Met 190	tat Tyr	ttc Phe	577
cgg ccc c Arg Pro L 1	tg acc eu Thr 95	agt Ser	tac Tyr	agt Ser	ctg Leu 200	aag Lys	cat His	gca Ala	ttg Leu	ata Ile 205	act Thr	gtg Val	atg Met	625
tac acg g Tyr Thr A 210														643
<210> 38 <211> 21 <212> PR <213> Mu	4	ulus	dom	esti	cus									
×222× (1	sc_fea )(64 xon =	3)		lone	= 0	R15-	71M2	1; A	cces	sion	DDB	J/EM	BL/GenBa	ink =
<400> 38	5													
Leu Val A	sp Ile	Phe 5	Phe	Ser	Ser	Val	Thr 10	Ile	Pro	Lys	Met	Leu 15	Ala	
Asn His L	eu Leu 20	ı Gly	Ser	Lys	Ala	Ile 25	Ser	Phe	Gly	Gly	Cys 30	Met	Ala	
Gln Met T	yr Phe	e Met	Ile	Ser	Leu 40	Gly	Asn	Thr	Asp	Ser 45	Tyr	Ile	e Leu	
Ala Ala M 50	Met Ala	a Tyr	· Asp	Arg 55	Ala	. Val	Ala	Ile	Ser 60	Arg	Pro	Leu	ı His	
Tyr Ala T	Chr Ile	e Met	Ser	Pro	Glr	Leu	. Cys	: Val	. Leu	. Let	. Val	Ala	Gly	

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Ser Trp Val I	le Ala Asn	Ala Asn	Ala Leu 1	Pro His Th	nr Leu Leu Thr
-	85		90		95

75

Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys 100

Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn 115 120

Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu 135

Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val 155

Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His

Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe

Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met 200

Tyr Thr Ala Val Thr Pro 210

<210> 386 <211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc\_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR15-71M24; Accession DDBJ/EMBL/GenBank = AF073967

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<221> CDS

<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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aac ttg ctg aca cag aga aag aca atc ctc ttt gcc cag tgc ctc act Asn Leu Leu Thr Gln Arg Lys Thr Ile Leu Phe Ala Gln Cys Leu Thr 25

caa atg tat ttc ttt gtg gct ttt ggt att aca gac agt ttc ctt ttg 145

Gln Met Tyr 35	Phe Phe	Val Ala	Phe Gl	y Ile	Thr	Asp	Ser 45	Phe	Leu	Leu	
gct gcg atg Ala Ala Met 50	gcc att Ala Ile	gac cgc Asp Arg 55	tat gt Tyr Va	t gct l Ala	att Ile	tgc Cys 60	aat Asn	ccg Pro	ctt Leu	cat His	193
tac aac aca Tyr Asn Thr 65	gtc atg Val Met	agt ccc Ser Pro 70	agg cg Arg Ar	c tgt g Cys	cgc Arg 75	ttg Leu	ctg Leu	gtt Val	gtg Val	gca Ala 80	241
tcc tgg gca Ser Trp Ala	gtg tcc Val Ser 85	cat ctt His Leu	cac tc His Se	c ctc r Leu 90	acc Thr	cac His	aca Thr	att Ile	ctc Leu 95	atg Met	289
ggt cgc ctc Gly Arg Leu	tct ttc Ser Phe	tgt gga Cys Gly	ccc aa Pro As 10	n Val	att Ile	cat His	cac His	ttc Phe 110	ttt Phe	tgt Cys	337
gat gtc cag Asp Val Gln 115	Pro Leu	ctg aca Leu Thr	ctc tc Leu Se 120	c tgc r Cys	tct Ser	gac Asp	acc Thr 125	tct Ser	atc Ile	aat Asn	385
gag ctc ttg Glu Leu Leu 130	gcc ttc Ala Phe	aca gag Thr Glu 135	Gly Se	t gtt r Val	gta Val	atc Ile 140	atg Met	agc Ser	cct Pro	ttt Phe	433
atc tta tto Ile Leu Leu 145	g ttg tct Leu Ser	ctt ata Leu Ile 150	tct at Ser Il	a ttc e Phe	act Thr 155	cgg Arg	act Thr	gtt Val	ctg Leu	agg Arg 160	481
gtc cct tca Val Pro Ser	ggg gaa Gly Glu 165	Gly Arg	tac aa Tyr Ly	a gtt s Val 170	Phe	tct Ser	acc Thr	tgt Cys	999 Gly 175	tct Ser	529
cac ctc aca His Leu Thi	gtt gta Val Val	a gca cto L Ala Leu	ttc ta Phe Ty 18	r Gly	acc Thr	ata Ile	ata Ile	tca Ser 190	gtg Val	tac Tyr	577
att cgc ccc Ile Arg Pro	Ser Ser	acc tac Thr Tyr	tca gt Ser Va 200	g aca l Thr	aag Lys	gac Asp	cga Arg 205	gtt Val	gtc Val	act Thr	625
gtc atc tat Val Ile Tyr 210	t aca gta r Thr Val	a gtt acc l Val Thi 215	Pro								649
<210> 387 <211> 216 <212> PRT <213> Mus	musculus	s domesti	cus						3		
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<400> 387											
Leu Val As	p Ile Cys 5	s Phe Th	Thr Va	al Ile 10	val	Pro	Gln	Met	Leu 15	Val	

Asn Leu Leu Thr Gln Arg Lys Thr Ile Leu Phe Ala Gln Cys Leu Thr

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Gln	Met	Tyr	Phe	Phe	Val	Ala	Phe	Gly	Ile	Thr	Asp	Ser	Phe	Leu	Leu
		35					40	_				45			

Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu His

Tyr Asn Thr Val Met Ser Pro Arg Arg Cys Arg Leu Leu Val Val Ala

Ser Trp Ala Val Ser His Leu His Ser Leu Thr His Thr Ile Leu Met 85

Gly Arg Leu Ser Phe Cys Gly Pro Asn Val Ile His His Phe Phe Cys 105 100

Asp Val Gln Pro Leu Leu Thr Leu Ser Cys Ser Asp Thr Ser Ile Asn 120 125

Glu Leu Leu Ala Phe Thr Glu Gly Ser Val Val Ile Met Ser Pro Phe

Ile Leu Leu Ser Leu Ile Ser Ile Phe Thr Arg Thr Val Leu Arg 150

Val Pro Ser Gly Glu Gly Arg Tyr Lys Val Phe Ser Thr Cys Gly Ser 170 165

His Leu Thr Val Val Ala Leu Phe Tyr Gly Thr Ile Ile Ser Val Tyr 180

Ile Arg Pro Ser Ser Thr Tyr Ser Val Thr Lys Asp Arg Val Val Thr 205 195

Val Ile Tyr Thr Val Val Thr Pro 210

<210> 388 <211> 649 <212> DNA

<213> Mus musculus domesticus

<220>

<221> misc feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR18M; Accession DDBJ/EMBL/GenBank = AF073968

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg aca Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr 20 25 30	97
caa atg tac ttt ttc agt gtt ttt gga agt ctg gag ata ttc ctt ctt Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 35 40 45	145
gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt caa Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln 50 55 60	193
tat tcc agc atc atg agc ccc aat ctc tgt gtg tgt gtg gtg ttc Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 65 70 75 80	241
tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc ttg Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu 85 90 95	289
gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc tgt Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110	337
gac ata tct gcc ctt ctg aag ttg gca tgc tct gat gtt tat att aat Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125	385
gaa tta atg ata ctt atc ttg gga ggg ttt ctt ctt gtc atc tca ctc Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 135 140	433
tta ctc atc att gta tcc tat gta caa att gtc tcc tca att tta agg Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160	481
att tot tot act ogg got ato cat aag oto tto too aco tgt ggo toa Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175	529
cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt ctg tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	577
tta tgt cca tca gct aat aac tct act gaa aag gag act gcc atg tcc Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 200 205	625
ctg atg tac aca gtg gtg act ccc Leu Met Tyr Thr Val Val Thr Pro 210 215	649
<210> 389 <211> 216 <212> PRT <213> Mus musculus domesticus	
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<222> (1)..(649)
<223> Taxon = 10092; clone = OR18M; Accession DDBJ/EMBL/GenBank = AF073968
<400> 389

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln 1 5 10 15

Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr 20 25 30

Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 35 40 45

Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln 50 55 60

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 65 70 75 80

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu 85 90 95

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125

Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 135 140

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 200 205

Leu Met Tyr Thr Val Val Thr Pro

<210> 390

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220 <221 <222 <223	> m > (	1)	feat (649 = 1	)	; cl	one	= OR	1M;	Acce	ssio	n DD	BJ/E	MBL/	GenB	ank =	AF073969
<220 <221 <222 <223 TM2	> C > ( > P	rodu	(649 ct =	) olf	acto	ry r	ecep	tor;	reg	ion	betw	een	tran	smem	brane	domains
<400 c tt Ph 1	c tc	90 t ga r As	t ct p Le	c tg u Cy 5	jc tt 's Ph	t tc .e Se	c tc r Se	t gt r Va	c ac l Th 10	r Me	g cc t Pr	c aa o Ly	a tt s Le	g ct u Le 15	g cag u Gln	49
aat Asn	ata Ile	cag Gln	agc Ser 20	cag Gln	gac Asp	cca Pro	tcc Ser	atc Ile 25	ccc Pro	tat Tyr	gca Ala	ggc Gly	tgc Cys 30	ctg Leu	gca Ala	97
caa Gln	aca Thr	tac Tyr 35	ttc Phe	ttt Phe	atg Met	gtt Val	ttt Phe 40	gga Gly	gat Asp	atg Met	gag Glu	agc Ser 45	ttc Phe	ctt Leu	ctt Leu	145
gtg Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctg Leu	cat His	193
tac Tyr 65	acc Thr	agc Ser	atc Ile	atg Met	agt Ser 70	ccc Pro	aaa Lys	ctc Leu	tgt Cys	ggt Gly 75	tgt Cys	cta Leu	atg Met	ctg Leu	cta Leu 80	241
ttg Leu	tgg Trp	atg Met	cta Leu	aca Thr 85	aca Thr	tcc Ser	cat His	gcc Ala	atg Met 90	atg Met	cat His	act Thr	ctc Leu	ctt Leu 95	gca Ala	289
gca Ala	aga Arg	ttg Leu	tct Ser 100	ttt Phe	tgt Cys	gag Glu	aac Asn	aat Asn 105	gțg Val	atc Ile	ctc Leu	aat Asn	ttt Phe 110	ttc Phe	tgt Cys	337
gac Asp	cta Leu	ttt Phe 115	gtt Val	ctc Leu	cta Leu	aag Lys	ctg Leu 120	gct Ala	tgc Cys	tca Ser	gac Asp	act Thr 125	tat Tyr	gtt Val	aat Asn	385
gag Glu	ttg Leu 130	atg Met	ata Ile	ttt Phe	ata Ile	atg Met 135	agt Ser	tcc Ser	ctc Leu	ctc Leu	att Ile 140	gtt Val	att Ile	cca Pro	ttt Phe	433
ttc Phe 145	ctc Leu	att Ile	gtc Val	atg Met	tct Ser 150	tat Tyr	gca Ala	agg Arg	atc Ile	att Ile 155	gcc Ala	tcc Ser	att Ile	ctt Leu	aag Lys 160	481
gtt Val	cca Pro	tct Ser	att Ile	caa Gln 165	Gly	atc Ile	tac Tyr	aag Lys	gtc Val 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	ggt Gly 175	tcc Ser	529
cat His	ctg Leu	tct Ser	gtg Val 180	gtg Val	acc Thr	ttg Leu	ttt Phe	tat Tyr 185	Gly	aca Thr	att Ile	att Ile	ggt Gly 190	Leu	tac Tyr	577
tta Leu	tgt Cys	cca Pro 195		ggt Gly	aat Asn	aat Asn	tcc Ser 200	Thr	gta Val	aag Lys	ggg Gly	act Thr 205	vai	atg Met	gcc Ala	625
atg Met	atg Met	tac Tyr	aca Thr	gtg Val	gtg Val	act Thr	ccc Pro									649

- <210> 391

- <211> 216 <212> PRT <213> Mus musculus domesticus
- <220>
- <221> misc\_feature
- <222> (1)..(649)
  <223> Taxon = 10092; clone = OR1M; Accession DDBJ/EMBL/GenBank = AF073969

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln

Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala

Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu 75

Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala

Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys

Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn

Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe

Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys 150 145

Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser 165

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180

Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala 200

## Met Met Tyr Thr Val Val Thr Pro 210 215

<210> 392 <211> 649 <212> DNA <213> Mus musculus domesticus	
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aat ata cag aca aag aac aag gtg ata acc tat gaa ggt tgc att tct  Asn Ile Gln Thr Lys Asn Lys Val Ile Thr Tyr Glu Gly Cys Ile Ser  20 25 30	
caa gta ttc ttt ttc ata cta ttt gga gtt tta gat aac ttt ctt cta Gln Val Phe Phe Phe Ile Leu Phe Gly Val Leu Asp Asn Phe Leu Leu 35 40 45	
gct gtg atg gcc tat gac cga tat gtg gca atc tgt cac cct ctg cac  Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His  50  55  60	
tat atg gtc atc atg aac cgc cgc ctc tgt gga ttt tta gtt ttg ggg  Tyr Met Val Ile Met Asn Arg Arg Leu Cys Gly Phe Leu Val Leu Gly  70  75  80	
tct tgg gtc aca aca gca ttg aat tcc ttg ctg cag agt tca atg gca 289 Ser Trp Val Thr Thr Ala Leu Asn Ser Leu Leu Gln Ser Ser Met Ala 85 90 95	
ctg cgg ctg tcc ttt tgt aca gac ttg aaa att ccc cac ttt gtt tgt Leu Arg Leu Ser Phe Cys Thr Asp Leu Lys Ile Pro His Phe Val Cys 100 105 110	
gag ctt aat caa ctg gta cta ctt gcc tgt aat gac acc ttt cct aat 385 Glu Leu Asn Gln Leu Val Leu Leu Ala Cys Asn Asp Thr Phe Pro Asn 115 120 125	
gac atg gtg atg tac ttt gca gct ata ctg ctg ggt ggt ggt cct ctt  Asp Met Val Met Tyr Phe Ala Ala Ile Leu Leu Gly Gly Pro Leu  130  135  140	
gct ggc atc ctt tac tct tat tct aag ata gtt tcc tcc ata cgt gca Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160	
atc tca tca cag ggg aag tat aaa gca tcc tcc acc tgt gca tcc  Ile Ser Ser Ser Gln Gly Lys Tyr Lys Ala Ser Ser Thr Cys Ala Ser  165 170 175	

cac ctc tca gtt gtt tca tta ttc tat tct aca ctc ttg ggt gcg tat  His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala Tyr  180 185 190	
ctt agt tct tct ttt aca caa aac tca cac tca act gca cga gca tct Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser 195 200 205	
gtt atg tac agt gtg gtc acc ccc Val Met Tyr Ser Val Val Thr Pro 210 215	
<210> 393 <211> 216 <212> PRT <213> Mus musculus domesticus	
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<400> 393	
Phe Ala Asp Ile Cys Phe Thr Ser Ala Ser Ile Pro Lys Met Leu Val 1 10 15	•
Asn Ile Gln Thr Lys Asn Lys Val Ile Thr Tyr Glu Gly Cys Ile Ser 20 25 30	
Gln Val Phe Phe Phe Ile Leu Phe Gly Val Leu Asp Asn Phe Leu Leu 35 . 40 45	
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50 55 60	
Tyr Met Val Ile Met Asn Arg Arg Leu Cys Gly Phe Leu Val Leu Gly 65 70 75 80	
Ser Trp Val Thr Thr Ala Leu Asn Ser Leu Leu Gln Ser Ser Met Ala 85 90 95	
Leu Arg Leu Ser Phe Cys Thr Asp Leu Lys Ile Pro His Phe Val Cys 100 105 110	
Glu Leu Asn Gln Leu Val Leu Leu Ala Cys Asn Asp Thr Phe Pro Asn 115 120 125	
Asp Met Val Met Tyr Phe Ala Ala Ile Leu Leu Gly Gly Gly Pro Leu 130 135 140	
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160	
Ile Ser Ser Ser Gln Gly Lys Tyr Lys Ala Ser Ser Thr Cys Ala Ser	

His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala Tyr
180 185 190

Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser 195 200 205

Val Met Tyr Ser Val Val Thr Pro 210 215

<210> 394
<211> 649
<212> DNA
<213> Mus musculus domesticus

<220>
<221> misc\_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR22M; Accession DDBJ/EMBL/GenBank = AF073971

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains
TM2 and TM7

<400> 394

<pr

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Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1 5 10 15

aac atg cag agc cag gac tca tcc atc acc tat gca gga tgc ctg aca 97
Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr
20 25 30

caa atg tac ttt ttc ttg ctc ttt gga gac ctt gag agc ttc ctc ctt 145 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu 35 40 45

gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc ccc ctt cat
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

tac atg agc atc atg agc ccc agc ctc tgt gtg agt ctg gtg ctg ctg
Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu
65 70 75 80

tcc tgg gtg ctg acc act ttc cat gcc atg ctg cat acc ctg ctc atg
Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
85 90 95

gcc aga ttg tca ttc tgt gag gac aat gtg atc ccc tac ttt ttc tgt
Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro Tyr Phe Phe Cys
100 105 110

gac atg tct gct ctg ctg aag ctg tcc tgc tct gac act cac gtt aat
Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
115 120 125

gaa ttg gtg ata ttt gtc aca gga ggc ctg atc ctt gtc att cca ttt 433 Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe

130 135 140 gtg ctc atc ctt gtg tcc tat gca cga att gtg tcc tcc att ctc aag 481 Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys gtc ccg tct gct cga ggc atc cgt aaa gcc ttc tcc acc tgt ggg tcc 529 Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 170 165 cac ctg tct gtg gtg tca ctg ttc tat ggg aca atc att ggt ctg tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 577 180 tta tgt cca tca gct gat aac tct act gtg aag gaa act gtc atg gcc Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala 625 200 195 649 atg atg tac aca gtg gtg act ccc Met Met Tyr Thr Val Val Thr Pro 215 <210> 395 <211> 216 <212> PRT <213> Mus musculus domesticus <220> <221> misc\_feature <222> (1)..(649) Taxon = 10092; clone = OR22M; Accession DDBJ/EMBL/GenBank = AF073971 <223> <400> 395 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His

Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu

70

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met 85 90 95

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro Tyr Phe Phe Cys 100 105 110

Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn 115 120 125

Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe 130 135 140												
Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 145 150 155 160												
Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175												
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190												
Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala 195 200 205												
Met Met Tyr Thr Val Val Thr Pro 210 215												
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c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49 Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln												
C ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa  Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln  1 5 10 15  aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca  Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala												
C ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa  Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln  1												
C ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa  Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln  1												

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110													
gac ctt tct gct ctc ctg aag ctg gcc tgc tct gat att cac att aat Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125													
gag tta atg ata atg ata att gga gca ctt gtt gtt ata ctt cca ttt Glu Leu Met Ile Met Ile Gly Ala Leu Val Val Ile Leu Pro Phe 130 135 140													
cta ctc atc ata gtg tct tat gcg cac att gtc tcc tcc att ctc aaa Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys 145 150 155 160													
gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggg tct Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175													
cat ctg tct gtg gtg tca ctg ttc tat ggg tca gtc att gtt ctg tac  His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr  180 185 190													
tta tgt cca tca tct aat aac tct act gtg aag gat act gtc atg tct Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 195 200 205													
atg atg tac act gtg gtg att ccc Met Met Tyr Thr Val Val Ile Pro 210 215													
<210> 397 <211> 216 <212> PRT <213> Mus musculus domesticus													
<212> PRT													
<212> PRT	72												
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<pre> &lt;212&gt; PRT &lt;213&gt; Mus musculus domesticus  &lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(649) &lt;223&gt; Taxon = 10092; clone = OR25M; Accession DDBJ/EMBL/GenBank = AF0739  &lt;400&gt; 397  Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln 1</pre>	72												
<pre> &lt;212&gt; PRT &lt;213&gt; Mus musculus domesticus  &lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(649) &lt;223&gt; Taxon = 10092; clone = OR25M; Accession DDBJ/EMBL/GenBank = AF0739  &lt;400&gt; 397  Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln 1</pre>	72												



Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 105

90

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys 150

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr 185

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 205 200

Met Met Tyr Thr Val Val Ile Pro

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<211> 649

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<213> Mus musculus domesticus

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<221> misc\_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR27M; Accession DDBJ/EMBL/GenBank = AF073973

<220>

<221> CDS

<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 398

c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49 Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln 5

aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca 97 Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala

caa atg tac ttc ttt ttg ttt ttt ggt gat gtt gag agt tta ctc ctt 145 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu

gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc tcc cct ctt cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His 193

	50					JJ					00						
tat Tyr 65	acc Thr	aga Arg	atc Ile	atg Met	agc Ser 70	cca Pro	aac Asn	ctc Leu	tgt Cys	gtg Val 75	agt Ser	atg Met	gtg Val	ctg Leu	ctg Leu 80	24	1
tcc Ser	tgg Trp	gca Ala	ctg Leu	aca Thr 85	aca Thr	ttg Leu	tat Tyr	gcc Ala	atg Met 90	ttg Leu	cac His	act Thr	ttg Leu	ctc Leu 95	tta Leu	28	9
act Thr	agg Arg	ttg Leu	tct Ser 100	ttc Phe	tgt Cys	aaa Lys	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	33	7
gac Asp	ctt Leu	tct Ser 115	gct Ala	ctc Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn	38	5
gag Glu	tta Leu 130	atg Met	ata Ile	atg Met	ata Ile	att Ile 135	gga Gly	gca Ala	ctt Leu	gtt Val	gtt Val 140	ata Ile	ctt Leu	cca Pro	ttt Phe	43	3
cta Leu 145	ctc Leu	atc Ile	ata Ile	gtg Val	tct Ser 150	tat Tyr	gcg Ala	cac His	att Ile	gtc Val 155	tcc Ser	tcc Ser	act Thr	ctc Leu	aaa Lys 160	48	1
gtc Val	cct Pro	tca Ser	act Thr	cga Arg 165	ggc Gly	atc Ile	cac His	aag Lys	gtc Val 170	ttc Phe	tcc Ser	act Thr	tgt Cys	ggt Gly 175	tct Ser	52	9
cat His	ctg Leu	tct Ser	gtg Val 180	Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly 333	tca Ser	gtc Val	att Ile	gtt Val 190	ctg Leu	tac Tyr	57	7
tta Leu	tgt Cys	cca Pro 195	Ser	tct Ser	aat Asn	aac Asn	tct Ser 200	Thr	gtg Val	aag Lys	gat Asp	act Thr 205	vaı	atg Met	tct Ser	62	:5
atg Met	atg Met 210	Tyr	act Thr	gtg Val	gtg Val	act Thr 215	Pro									64	19
<21 <21 <21 <21	1> 2>	399 216 PRT Mus	musc	ulus	dom	esti	cus										
<22 <22 <22 <22	1>	(1)	-164	ture 9) 1009		lone	· = 0	R27M	i; Ac	cess	ion	DDBJ	/EME	BL/Ge	nBank	= AFO	7397:
< 40	0>	399															

Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln 1 5 10 15

Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu 35 40 45

- Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His
- Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
- Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
- Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
- Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
- Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
- Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Thr Leu Lys 145
- Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 170 165
- His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr 185 180
- Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 200
- Met Met Tyr Thr Val Val Thr Pro
- <210> 400
- <211> 649
- <212> DNA
- <213> Mus musculus domesticus
- <220>
- <221> misc\_feature
- <222> (1)...(649)
- <223> Taxon = 10092; clone = OR28M; Accession DDBJ/EMBL/GenBank = AF073974
- <220>
- <221> CDS
- (2)..(649) <222>
- <223> Product = olfactory receptor; region between transmembrane domains
- <400> 400
- 49 a gtg gtg gac atc tgc tac acc tcc agt ggg gtc ccc cag atg ctg gca Val Val Asp Ile Cys Tyr Thr Ser Ser Gly Val Pro Gln Met Leu Ala 10

cac His	ttc Phe	ctc Leu	atg Met 20	gag Glu	aaa Lys	aag Lys	acc Thr	atc Ile 25	tct Ser	ttt Phe	gcc Ala	cta Leu	tgt Cys 30	Gly ggg	acc Thr		97
cag Gln	ctc Leu	ttc Phe 35	ttt Phe	gct Ala	ctg Leu	act Thr	ctt Leu 40	ggg Gly	gga Gly	act Thr	gag Glu	ttt Phe 45	ctg Leu	ttg Leu	ctg Leu		145
act Thr	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gct Ala	gtc Val	tgt Cys 60	aat Asn	cca Pro	tta Leu	cgg Arg		193
tac Tyr 65	aca Thr	gtg Val	gtg Val	atg Met	aac Asn 70	cca Pro	agg Arg	ctc Leu	tgc Cys	atg Met 75	ggt Gly	cta Leu	gca Ala	ggt Gly	gtc Val 80		241
tct Ser	tgg Trp	ttt Phe	gtg Val	ggt Gly 85	gta Val	gtt Val	aat Asn	tct Ser	gct Ala 90	gtg Val	gag Glu	aca Thr	gca Ala	gtc Val 95	acc Thr		289
atg Met	tac Tyr	ctt Leu	ccc Pro 100	acc Thr	tgt Cys	Gly ggg	cac His	aat Asn 105	gta Val	ctc Leu	aac Asn	cat His	gtg Val 110	gcc Ala	tgt Cys		337
gag Glu	aca Thr	ctg Leu 115	gca Ala	ctg Leu	gtc Val	aga Arg	ctg Leu 120	gcc Ala	tgt Cys	gtg Val	gac Asp	atc Ile 125	acc Thr	ctc Leu	aac Asn		385
caa Gln	gtg Val 130	gtg Val	ata Ile	ctg Leu	gct Ala	tct Ser 135	agt Ser	gtg Val	gtg Val	gtg Val	ctg Leu 140	atg Met	ata Ile	ccc Pro	tgc Cys		433
tct Ser 145	ctg Leu	gtc Val	tct Ser	ctg Leu	tcc Ser 150	tat Tyr	gcc Ala	cac His	att Ile	gta Val 155	gct Ala	gcc Ala	atc Ile	atg Met	aag Lys 160		481
atc Ile	cgt Arg	tct Ser	acc Thr	cag Gln 165	gga Gly	cgc Arg	cgc Arg	aaa Lys	gcc Ala 170	ttt Phe	gag Glu	acc Thr	tgt Cys	gcc Ala 175	tcc Ser		529
cat His	ctg Leu	act Thr	gtg Val 180	gtc Val	tcc Ser	atg Met	tct Ser	tat Tyr 185	ggg ggg	atg Met	gcc Ala	ctc Leu	ttc Phe 190	Thr	tac Tyr		577
ctg Leu	Gln	cct Pro 195	Ala	Ser	Thr	gcc Ala	Ser	Ala	Glu	Gln	gac Asp	Lys	Val	gta Val	gtg Val		625
atc Ile	ttc Phe 210	Tyr	gct Ala	ttg Leu	gtc Val	acc Thr 215	ccc Pro										649
<210 <211 <212	l >	401 216 PRT															
<213			musc	ulus	dom	esti	cus										
<220 <220 <220 <220	1>	(1)	. (64	ture 9) 1009		lone	= 0	R28M	; Ac	cess:	ion	DDBJ	/EME	sL/Ge	nBank	s = A	F073974
<40	0 >	401															
W-1	T/al	λαν	Tle	Cve	ተ ጥህን	Thr	Ser	Ser	Glv	v Val	Pro	Gln	Met	. Leu	Ala		

Val Val Asp Ile Cys Tyr Thr Ser Ser Gly Val Pro Gln Met Leu Ala

His Phe Leu Met Glu Lys Lys Thr Ile Ser Phe Ala Leu Cys Gly Thr 20 25 30

Gln Leu Phe Phe Ala Leu Thr Leu Gly Gly Thr Glu Phe Leu Leu 40 45

Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg 50 60

Tyr Thr Val Val Met Asn Pro Arg Leu Cys Met Gly Leu Ala Gly Val
65 70 75 80

Ser Trp Phe Val Gly Val Val Asn Ser Ala Val Glu Thr Ala Val Thr 85 90 95

Met Tyr Leu Pro Thr Cys Gly His Asn Val Leu Asn His Val Ala Cys 100 105 110

Glu Thr Leu Ala Leu Val Arg Leu Ala Cys Val Asp Ile Thr Leu Asn 115 120 125

Gln Val Val Ile Leu Ala Ser Ser Val Val Val Leu Met Ile Pro Cys 130 135 140

Ser Leu Val Ser Leu Ser Tyr Ala His Ile Val Ala Ala Ile Met Lys 145 150 155 160

Ile Arg Ser Thr Gln Gly Arg Arg Lys Ala Phe Glu Thr Cys Ala Ser 165 170 175

His Leu Thr Val Val Ser Met Ser Tyr Gly Met Ala Leu Phe Thr Tyr 180 185 190

Leu Gln Pro Ala Ser Thr Ala Ser Ala Glu Gln Asp Lys Val Val Val 195 200 205

Ile Phe Tyr Ala Leu Val Thr Pro 210 215

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<220>

<221> CDS <222> (2)(649) <223> Product = olfactory receptor; region between transmembrane TM2 and TM7	domains												
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aaa ttt gtc atg gtg aag agt gtc att tct ttt gca gaa tgc atg gct Lys Phe Val Met Val Lys Ser Val Ile Ser Phe Ala Glu Cys Met Ala 20 25 30	97												
cag ttt tac tta ttt gat gtt ttt gct gtt tca gag tgt cac atg ctg Gln Phe Tyr Leu Phe Asp Val Phe Ala Val Ser Glu Cys His Met Leu 35 40 45	145												
gct gtc atg gct tat gat cgc tat gtt gcc atc tgt aac ccc ttg cta Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu 50 55 60	193												
tat aat gtt acc atg tct tac aaa gtg tgt tcc tgg atg gta gtg ggg Tyr Asn Val Thr Met Ser Tyr Lys Val Cys Ser Trp Met Val Val Gly 65 70 75 80	241												
gtg tat agt gta ggc ttg att tgt gcc aca ggg gaa aca gtc tgc ctg Val Tyr Ser Val Gly Leu Ile Cys Ala Thr Gly Glu Thr Val Cys Leu 85 90 95	289												
ctt aga ctg cta ttc tgc aaa gct gat gac ata aac cac tac ttc tgt Leu Arg Leu Leu Phe Cys Lys Ala Asp Asp Ile Asn His Tyr Phe Cys 100 105 110	337												
gat ctt tta cca cta ctg gaa caa tcc tgt tcc aat aca ttt atc aat Asp Leu Leu Pro Leu Leu Glu Gln Ser Cys Ser Asn Thr Phe Ile Asn 115 120 125	385												
gaa ata cta gga ctg tcc ttc agt tca ttt aat act act gtc cca gct Glu Ile Leu Gly Leu Ser Phe Ser Ser Phe Asn Thr Thr Val Pro Ala 130 135 140	433												
ctg acc atc ctc agt tcc tac atc ttc atc ata gcc agc atc ctc cgc Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser Ile Leu Arg 145 150 160	481												
att cct tcc act gaa ggc agg tcc aaa gcc ttc agc acc tgc agc tcc Ile Pro Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175	529												
cac atc ttg gct gtt gct gtc ttc ttt ggg tct tta gca ttc atg tac His Ile Leu Ala Val Ala Val Phe Phe Gly Ser Leu Ala Phe Met Tyr 180 185 190	577												
ctt cag cca tca tca gtc agc tcc atg gac caa ggg aaa gtg tcc tct Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys Val Ser Ser 195 200 205	625												
gtg ttt tat acc att gtt gtg ccc Val Phe Tyr Thr Ile Val Val Pro 210 , 215	649												
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<220>

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<222> (1)..(649)

<223> Taxon = 10092; clone = OR29M; Accession DDBJ/EMBL/GenBank = AF073975

<400> 403

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Lys Phe Val Met Val Lys Ser Val Ile Ser Phe Ala Glu Cys Met Ala 20 25 30

Gln Phe Tyr Leu Phe Asp Val Phe Ala Val Ser Glu Cys His Met Leu 35 40 45

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu 50 55 60

Tyr Asn Val Thr Met Ser Tyr Lys Val Cys Ser Trp Met Val Val Gly 65 70 75 80

Val Tyr Ser Val Gly Leu Ile Cys Ala Thr Gly Glu Thr Val Cys Leu 85 90 95

Leu Arg Leu Leu Phe Cys Lys Ala Asp Asp Ile Asn His Tyr Phe Cys 100 105 110

Asp Leu Leu Pro Leu Leu Glu Gln Ser Cys Ser Asn Thr Phe Ile Asn 115 120 125

Glu Ile Leu Gly Leu Ser Phe Ser Ser Phe Asn Thr Thr Val Pro Ala 130 135 140

Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser Ile Leu Arg 145 150 155 160

Ile Pro Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175

His Ile Leu Ala Val Ala Val Phe Phe Gly Ser Leu Ala Phe Met Tyr 180 185 190

Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys Val Ser Ser 195 200 205

Val Phe Tyr Thr Ile Val Val Pro

<210> 404

<211> 649 <212> DNA <213> Mus musculus domesticus													
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aac atg cag agc caa gtt cct tca atc ccc tat gca ggc tgc ctg aca  Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr  20 25 30	7												
caa atg tac ttc ttt ttg ttt ttt gga gat ctt gag agc ttc ctc ctt Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu 35 40 45	5												
gtg gcc atg gcc tat gac cga tat gta gcc atc tgc ttc cct ctt cat  Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His  50 55 60	13												
tac acc agc att atg agc ccc agg ctc tgt gtg agt ctt gtg ctg ctg Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu 65 70 75 80	:1												
tcc tgg ttg ctg acc atg tcc cat tcc atg ctg cac act ttg ctc tta 28 Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu 85 90 95	39												
act agg ttg tct ttc tgt gaa aac aat gtg atc ccc cat ttt ttc tgt Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110	37												
gat ctg tct gct ctg ctg aag ctg gcc tgc tct gat att cac att aat Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125	85												
gaa ttg gtg ata ttg atc ata gga ggg ctt gtt gtt ata ctt cca ttt 4: Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe 130 135 140	33												
cta ctc gtc aca gtg tct tat gca cgc atc atc tcc tcc att ctc aag Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys 145 150 155 160	81												
gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175	29												
cac ctg tct gtg gtg tca ctg ttc tat ggg aca att att ggc ctc tac 5 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	77												
tta tgt cca tct gct aat aac tct act cta aag gac act gtc atg tct 6 Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser	25												

195 200 205

ctg atg tac act gtg gta act ccc Leu Met Tyr Thr Val Val Thr Pro 649

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<212> PRT

<213> Mus musculus domesticus

<220>

<221> misc\_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR2M; Accession DDBJ/EMBL/GenBank = AF073976

<400> 405

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Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 20 25 30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu 35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 60

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu 65 70 75 80

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu 85 90 95

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Cys 100 105 110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe 130 135 140

Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys 145 150 155 160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

## Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 195 200 205

Leu Met Tyr Thr Val Val Thr Pro 210 215

<210><211><212><212><213>	406 650 DNA Mus n	nuscu	lus	dome	stic	us									
<220><221><222><222><223>	misc_ (1) Taxor	(650	)	; cl	one	= OR	.3M;	Acce	ssio	n DE	BJ/E	MBL/	GenB	ank =	AF073977
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<400> cc ttc Phe 1	406 tct g	gat c Asp I	tc teu C	ys P	tt t he S	.cc t Ser S	ct g Ser V	al T	ca a Thr M	itg d Met E	cc a	ag t ys I	eu I	etg Leu L5	47
cag aa Gln As	c atg n Met	cag Gln	atc Ile 20	cag Gln	gac Asp	aca Thr	ccc Pro	ata Ile 25	tcc Ser	tat Tyr	gtg Val	gct Ala	tgt Cys 30	ctg Leu	95
aca ca Thr Gl	a atg .n Met	tac Tyr 35	ttt Phe	ttc Phe	agt Ser	gtt Val	ttt Phe 40	gga Gly	agt Ser	ctg Leu	gag Glu	ata Ile 45	ttc Phe	ctt Leu	143
ctt gt Leu Va	a gtc al Val 50	ctg Leu	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgt Cys 60	tta Leu	ccc Pro	ctt Leu	191
caa ta Gln Ty 65	r Ser	agc Ser	atc Ile	atg Met	agc Ser 70	ccc Pro	aat Asn	ctc Leu	tgt Cys	gtg Val 75	tgt Cys	gtg Val	gtg Val	gtg Val	239
ttc to Phe Cy 80	gc tgg /s Trp	gta Val	ttt Phe	att Ile 85	gtg Val	ttt Phe	tat Tyr	gcc Ala	atg Met 90	ttt Phe	cac His	aca Thr	cta Leu	ctc Leu 95	287
ttg go Leu Al	ct aga la Arg	ttg Leu	tca Ser 100	ttt Phe	tgt Cys	aag Lys	aac Asn	aat Asn 105	gtg Val	atc Ile	cca Pro	cac His	ttt Phe 110	ttc Phe	335
tgt ga Cys As	ac ata sp Ile	tct Ser 115	gcc Ala	ctt Leu	ctg Leu	aag Lys	ttg Leu 120	gca Ala	tgc Cys	tct Ser	gat Asp	gtt Val 125	tat Tyr	att Ile	383
aat ga Asn G	aa tta lu Leu 130	Met	ata Ile	ctt Leu	atc Ile	ttg Leu 135	gga Gly	GJ A aaa	ttt Phe	ctt Leu	ctt Leu 140	gtc Val	acc Thr	tca Ser	431
Leu Le	ta ctc eu Leu 45	atc Ile	att Ile	gta Val	tcc Ser 150	Tyr	gta Val	caa Gln	att Ile	gtc Val 155	tcc Ser	tca Ser	att Ile	tta Leu	479

agg att tot tot act ogg got atc cat aag otc tto too acc tgt ggc Arg Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly 160 165 170 175	
tca cac ctg tct gtg gtc tca ctg ttc tat ggg gca att att ggt ctg Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu 180 185 190	
tac tta tgt cca tca gct aat aac tct act gaa aag gag act gcc atg Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met 195 200 205	
tcc ctg atg tac aca gtg gtg act ccc Ser Leu Met Tyr Thr Val Val Thr Pro 210 215	
<210> 407 <211> 216 <212> PRT <213> Mus musculus domesticus	
<pre>&lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(650) &lt;223&gt; Taxon = 10092; clone = OR3M; Accession DDBJ/EMBL/GenBank = AF0739</pre>	177
<400> 407	
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Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr 20 25 30	
Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 35 40 45	
Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln 50 55 60	
Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 65 70 75 80	
Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu 85 90 95	
Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110	
Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125	
Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Thr Ser Leu 130 135 140	
Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg	

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 200 205

Leu Met Tyr Thr Val Val Thr Pro

<210> 408 <211> 648 <212> DNA <213> Mus musculus domesticus

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<221> misc\_feature <222> (1)..(648)

<223> Taxon = 10092; clone = OR4M; Accession DDBJ/EMBL/GenBank = AF073978

<220>

<221> CDS

<222> (2)..(646)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr
20 25 30

caa atg tac ttt ttc agt gtt ttt ggg agt ctg gag ata ttc ctt ctt 145 Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 35 40 45

gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt caa 193
Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln
50 60

tat tcc agc atc atg agc ccc aat ctc tgt gtg tgt gtg gtg gtg ttc

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe
65 70 75 80

tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc ttg

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu

85 90 95

gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc tgt 337 Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110

gac ata tct gcc ctt ctg aag ttg gca tgc tct gat gtt tat att aat 385 Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn

115 120 125

:	115				120					125				
gaa tta a Glu Leu 1 130	atg at Met Il	a ctt e Leu	atc Ile	ttg Leu 135	gga Gly	Gly aaa	ttt Phe	ctt Leu	ctt Leu 140	gtc Val	atc Ile	tca Ser	ctc Leu	433
tta ctc a Leu Leu 1 145	atc at Ile Il	t gta e Val	tcc Ser 150	tat Tyr	gta Val	caa Gln	att Ile	gtc Val 155	tcc Ser	tca Ser	att Ile	tta Leu	agg Arg 160	481
att tct : Ile Ser :	tct ac Ser Th	t cgg r Arg 165	gct Ala	atc Ile	cat His	aag Lys	ctc Leu 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	ggc Gly 175	tca Ser	529
cac ctg	tct gt Ser Va 18	l Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly 999	aca Thr	att Ile	att Ile	ggt Gly 190	ctg Leu	tac Tyr	577
tta tgt Leu Cys	cca to Pro Se 195	a gct r Ala	aat Asn	aac Asn	tct Ser 200	act Thr	gaa Glu	aag Lys	gag Glu	act Thr 205	gcc Ala	atg Met	tcc Ser	625
ctg atg Leu Met 210	tac ac Tyr Th	a gtg r Val	gtg Val	act Thr 215	cc									648
<211> 2 <212> P	09 15 RT lus mus	culus	dome	esti	cus									
-222 (	nisc_fe 1)(6 axon =	(84)		lone	= O:	R4M;	Acc	essi	on Di	DBJ/	EMBL,	/Geni	Bank = AF	073978
<400> 4	.09													
Phe Ser 1	Asp Le	eu Cys 5	Phe	Ser	Ser	Val	Thr 10	Met	Pro	Lys	Leu	Leu 15	Gln	
Asn Met	Gln II		Asp	Thr	Pro	Ile 25	Ser	Tyr	Val	Ala	Cys 30	Leu	Thr	
Gln Met	Tyr Pl	ne Phe	Ser	Val	Phe	Gly	Ser	Leu	Glu		Phe	Leu	Leu	
					10					45	•			
Val Val 50		la Tyr	: Asp	Arg 55		Val	Ala	Ile	Cys 60		Pro	Leu	Gln	
	Leu A			55	Tyr				60	Leu				
50 Tyr Ser	Leu A	le Met	Ser 70	55 Pro	Tyr Asn	Leu	. Cys	Val	60 Cys	Leu Val	Val	Val	Phe 80	

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125	
Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 135 140	
Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160	
Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175	
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	
Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 200 205	
Leu Met Tyr Thr Val Val Thr 210 215	
<210> 410 <211> 649 <212> DNA <213> Mus musculus domesticus	
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aac atg cag agc cag gac cca tcc atc ccc tat gcc agc tgt ctg aca  Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Ser Cys Leu Thr  20 25 30	7
caa atg tac ttt ttc atg gct ttt ggg aac atg gaa att tat ctt ctt Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Met Glu Ile Tyr Leu Leu 35 40 45	5
gtg gtc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctt cat  Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His  50 55 60	3
tac acc agc atc atg agc cct aag ctc tgt gtg tct ctg gtg gtt ctc  Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu  65 70 75 80	1

tct tgg gta ttt acc att ctg tat tcc atg tta cac acc cta ctc ttg Ser Trp Val Phe Thr Ile Leu Tyr Ser Met Leu His Thr Leu Leu 85 90 95	289
gca aga ttg tca ttc tgt gag gac aat gtg atc ccc cac ttt ttc tgt Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys 100 105 110	337
gac ata tct gcc ctg ctc aag ttg gcc tgc tct gac att tct att aat Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Ser Ile Asn 115 120 125	385
gaa cta atg ata ttt atc gtg gga ggg ctt gat act gta atc cca ttt Glu Leu Met Ile Phe Ile Val Gly Gly Leu Asp Thr Val Ile Pro Phe 130 135 140	433
tta ctc att gtt gtt tcc tat gta caa att gtc tgc tcc att cta aag Leu Leu Ile Val Val Ser Tyr Val Gln Ile Val Cys Ser Ile Leu Lys 145 150 155 160	481
ttc tca tct aca cgg ggc ata cac aag gtc ttc tcc acc tgt ggc tcc Phe Ser Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175	529
cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt gtc tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr 180 185 190	577
ata tgc cca tca gct aat aac tct act gtg aag gag act gtc atg tcc Ile Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser 195 200 205	625
ctg atg tac aca gtg gtg acg ccc Leu Met Tyr Thr Val Val Thr Pro 210 215	649
<210> 411 <211> 216 <212> PRT <213> Mus musculus domesticus	
<pre>&lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (1)(649) &lt;223&gt; Taxon = 10092; clone = OR5M; Accession DDBJ/EMBL/GenBank</pre>	= AF073979
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Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Ser Cys Leu Thr 20 25 30	
Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Met Glu Ile Tyr Leu Leu 35 40 45	
Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60 `	
Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu	

Ser Trp Val Phe Thr Ile Leu Tyr Ser Met Leu His Thr Leu Leu Leu

70

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys 105

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Ser Ile Asn

Glu Leu Met Ile Phe Ile Val Gly Gly Leu Asp Thr Val Ile Pro Phe 130

Leu Leu Ile Val Val Ser Tyr Val Gln Ile Val Cys Ser Ile Leu Lys 150

Phe Ser Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 170

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr 190

Ile Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser 205

Leu Met Tyr Thr Val Val Thr Pro 210

<210> 412

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc\_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR6M; Accession DDBJ/EMBL/GenBank = AF073980

<220>

<221> CDS

<222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 412

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aac atg cag agc caa gtt cct tca atc ccc tat gca ggc tgc ctg aca 97 Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 25

caa atg tac ttc ttt ttg ttt ttt gga gat ctt gag agc ttc ctc ctt 145 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu

337 gat ctg tct gct ctg ctg aag ctg gcc tgc tct gat att cac att aat 385 Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 125 120 gaa ttg gtg ata ttg atc ata gga ggg ctt gtt gtt ata ctt cca ttt 433 Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe 135 cta ctc gtc aca gtg cct tat gca cgc atc atc tcc tcc att ctc aag 481 Leu Leu Val Thr Val Pro Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys 155 150 gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct 529 Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 175 165 cac ctg tct gtg gtg tca ctg ttc tat ggg aca att att ggc ctc tac 577 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 185 tta tgt cca tct gct aat aac tct act cta aag gac act gtc atg tct 625 Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 200

ctg atg tac act gtg gta act ccc
Leu Met Tyr Thr Val Val Thr Pro
210
215

<210> 413 <211> 216

<212> PRT

<213> Mus musculus domesticus

<220>

<221> misc feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR6M; Accession DDBJ/EMBL/GenBank = AF073980

<400> 413

Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Gln
1 10 15

Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 20 25 30

- Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
- Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55
- Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu 75
- Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
- Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 105 100
- Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
- Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe 130
- Leu Leu Val Thr Val Pro Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys 150
- Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170
- His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180
- Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 205
- Leu Met Tyr Thr Val Val Thr Pro 215
- <210> 414
- <211> 649
- <212> DNA
- <213> Mus musculus domesticus
- <220>
- <221> misc\_feature
- <222> (1)..(649)
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- <221> CDS
- <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7
- <400> 414

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aac atg Asn Met	cag agc Gln Ser 20	caa gt Gln Va	ta tca al Ser	tcc Ser	att Ile 25	ccc Pro	tat Tyr	gca Ala	ggc Gly	tgc Cys 30	ctt Leu	gca Ala	97
caa atg Gln Met	tac ttc Tyr Phe 35	ttt ti Phe Lo	tg ttt eu Phe	ttt Phe 40	ggt Gly	gat Asp	gtt Val	gag Glu	agc Ser 45	tta Leu	ctc Leu	ctt Leu	145
gtt gcc Val Ala 50	atg gcc Met Ala	tat ga Tyr A	ac cgt sp Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctt Leu	cat His	193
tat acc Tyr Thr 65	aga atc Arg Ile	atg ag Met S	er Pro	aac Asn	ctc Leu	tgt Cys	gtg Val 75	agt Ser	atg Met	gtg Val	ctg Leu	ctg Leu 80	241
tcc tgg Ser Trp	gca ctg Ala Leu	aca a Thr T 85	ca ttg hr Leu	tat Tyr	gcc Ala	atg Met 90	ttg Leu	cac His	act Thr	ttg Leu	ctc Leu 95	tta Leu	289
act agg Thr Arg	ttg tct Leu Ser 100	ttc t Phe C	gt aaa ys Lys	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	337
gac ctt Asp Leu	tct gct Ser Ala 115	ctc c Leu L	tg aag eu Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn	385
gag tta Glu Leu 130	atg ata Met Ile	atg a Met I	ta att le Ile 135	gga Gly	gca Ala	ctt Leu	gtt Val	gtt Val 140	ata Ile	ctt Leu	cca Pro	ttt Phe	433
cta ctc Leu Leu 145	atc ata Ile Ile	Val S	ct tat Ser Tyr .50	gcg Ala	cac His	att Ile	gtc Val 155	tcc Ser	tcc Ser	att Ile	ctc Leu	aaa Lys 160	481
gtc cct Val Pro	tca act Ser Thr	cga g Arg G 165	gc atc ly Ile	cac His	aag Lys	gtc Val 170	ttc Phe	tcc Ser	act Thr	tgt Cys	ggt Gly 175	tct Ser	529
cat ctg His Leu	tct gcg Ser Ala 180	Val S	ca ctg Ser Leu	ttc Phe	tat Tyr 185	Gly aaa	tca Ser	gtc Val	att Ile	gtt Val 190	ctg Leu	tac Tyr	577
tta tgt Leu Cys	cca tca Pro Ser 195	tct a	at aac Asn Asn	tct Ser 200	act Thr	gtg Val	aag Lys	gat Asp	act Thr 205	vaı	atg Met	tct Ser	625
atg atg Met Met 210	tac act Tyr Thr	gtg g Val V	gtg act Val Thr 215	Pro									649
		culus o	lomesti	cus									
-2225	misc_fea (1)(64 Taxon =	19)	; clone	e = C	R7M;	Acc	essi	on E	DBJ/	'EMBL	ı/Gen	ıBank =	AF073981

Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln

Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55

Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu 75

Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe 130

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys 145

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165

. His Leu Ser Ala Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 200

Met Met Tyr Thr Val Val Thr Pro 210

<210> 416

<211> 649

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aat ata cag agc cag gac cca tcc atc ccc tat gca ggc tgc ctg gca Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30	
caa aca tac ttc ttt atg gtt ttt gga gat atg gag agc ttc ctt ctt Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu 35 40 45	
gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctg cat 193 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60	)
tac acc agc atc atg agt ccc aaa ctc tgt ggt tgt cta atg ctg cta 241 Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu 65 70 75 80	•
ttg tgg atg cta aca aca tcc cat gcc atg atg cat act ctc ctt gca 289 Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala 85 90 95	)
gca aga ttg tct ttt tgt gag aac aat gtg atc ctc aat ttt ttc tgt 337 Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys 100 105 110	7
gac cta ttt gta ctc cta aag ctg gct tgc tca gac act tat gtt aat 385 Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 115 120 125	5
gag ttg atg ata ttt ata atg agt tcc ctc ctc att gtt att cca ttt 433 Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe 130 135 140	3
ttc ctc att gtc atg tct tat gca agg atc att gcc tcc att ctt aag  Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys  145 150 155 160	L
gtt cca tct att caa ggg atc tac aag gtc ttc tcc acc tgt ggt tcc 529 Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser 165 170 175	<b>Э</b>
cat ctg tct gtg gtg acc ttg ttt tat ggg aca att att ggt ctc tac 577 His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	7
tta tgt cca tca ggt aat aat tcc aca gta aag ggg act gtc atg gcc 625 Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala 195 200 205	5
atg atg tac aca gcg gtg act ccc  Met Met Tyr Thr Ala Val Thr Pro 210 215	9

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  <213> Mus musculus domesticus

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- Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30
- Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu 35 40 45
- Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60
- Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu 65 70 75 80
- Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala 85 90 95
- Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys 100 105 110
- Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn
- Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe 130 135 140
- Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys 145 150 155 160
- Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser 165 170 175
- His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190
- Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala 195 200 205
- Met Met Tyr Thr Ala Val Thr Pro

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<223> Product = olfactory receptor; region between transmembrane domains
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  Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
                                                                          97
aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc
Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser
cag atg tct gtc ttc ttg gtt ttt gca gaa ttg gac aac ttt ctc ctg
Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu
                                                                         145
                                                                         193
get gtg atg gee tat gae ega tat gtg get ate tgt cae eea tta tat
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
tac aca gtc att gtt aac caa cat ctc tgt ata ctg atg gtt ctg ctg
                                                                         241
Tyr Thr Val Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu
                     70
tee tgg gtt gtt age ate eta cat gee tte tta cag age tea att gtg
                                                                          289
Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val
                                      90
                                                                          337
cta cag ttg acc ttt tgt gga gat gta aaa att ccc cac ttc ttc tgt
Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys
                                  105
             100
                                                                          385
gag ctt aac cag ctg tct caa ctc aca tgt tca gac agc ttt tca agc
Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Phe Ser Ser
                                                   125
caa ctc ata atg aat ctt gta cct gtt cta ttg gca gtc att tcc ttc
                                                                          433
Gln Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe
                          135
agt agt atc ctt tac tct tat ttc aag ata gtg tcc tcc ata tgt tct
                                                                          481
Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser
                     150
atc tcc tca gtt caa ggg aag tac aag gca ttt tct aca tgt gtc tct
                                                                          529
Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
                                       170
cac ctt tcc att gtc tcc tta ttt tat agt aca ggc ctt gga gtg tat
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His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr
           180
                                185
gtc agt tot gtt gtg atc caa agc tot cac tot gct gca aga gcc tot
                                                                      625
Val Ser Ser Val Val Ile Gln Ser Ser His Ser Ala Ala Arg Ala Ser
                            200
                                                                       649
gtg atg tat act gtg gtc acc ccg
Val Met Tyr Thr Val Val Thr Pro
    210
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<211> 216
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<213> Mus musculus domesticus
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AF073983
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Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser
                                 25
            20
Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu
                             40
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
    50
Tyr Thr Val Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu
Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val
Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys
                                 105
Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Phe Ser Ser
         115
                             120
 Gln Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe
     130
 Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser
                     150
 145
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Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser

His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr

Val Ser Ser Val Val Ile Gln Ser Ser His Ser Ala Ala Arg Ala Ser

Val Met Tyr Thr Val Val Thr Pro

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<211> 646

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<220>

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<223> Taxon = 10092; clone = OR912-47M6; Accession DDBJ/EMBL/GenBank = AF073984

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<221> CDS

(2)..(646) <222>

<222> (2)..(040) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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att cac ata cta aga aat caa gcc att tcg ttc tct ggg tgc ctc aca 97 Ile His Ile Leu Arg Asn Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr 25

145 cag ctg tat ttt ctc tgt gtg ttt gct gac atg gac aat ttc ctg ctg Gln Leu Tyr Phe Leu Cys Val Phe Ala Asp Met Asp Asn Phe Leu Leu 35

193 gct gtg atg gcc tat gac cga ttt gtg gcc ata tgc cac cct tta cac Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55

241 tac aca aca aag atg acc cat cag ctt tgt gcc ttt ctt gtt ggg Tyr Thr Thr Lys Met Thr His Gln Leu Cys Ala Phe Leu Val Val Gly 70

tcc tgg atg gta gcc agt ctg aat gct ctg ttg cac aca ctg ctc gtg 289 Ser Trp Met Val Ala Ser Leu Asn Ala Leu Leu His Thr Leu Leu Val 90

get caa etc tac tte tgt ggg gac aat gtg ate eee cae tte tte tgt 337 Ala Gln Leu Tyr Phe Cys Gly Asp Asn Val Ile Pro His Phe Phe Cys

gaa gtg act ccc ctg ctg aaa ctc tct tgc tca gac aca cat ctc aat 385 Glu Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn 115 125

gag ttg atg att ctt gct gtt gca ggg ctg ata atg tta gct cca ttt 433

Glu	Leu 130	Met	Ile	Leu	Ala	Val 135	Ala	Gly	Leu	Ile	Met 140	Leu	Ala	Pro	Phe	
gtt Val 145	tgc Cys	atc Ile	ctc Leu	ttg Leu	tct Ser 150	tat Tyr	atc Ile	ctt Leu	att Ile	gct Ala 155	tgt Cys	gcc Ala	atc Ile	ctg Leu	aaa Lys 160	481
atc Ile	tca Ser	tcc Ser	aca Thr	gga Gly 165	aga Arg	tgg Trp	aaa Lys	gcc Ala	ttc Phe 170	tct Ser	acc Thr	tgt Cys	ggc Gly	tca Ser 175	cac His	529
ttg Leu	gct Ala	gtt Val	gtg Val 180	tgc Cys	ctc Leu	ttc Phe	tat Tyr	ggc Gly 185	act Thr	atc Ile	ata Ile	tcc Ser	ctg Leu 190	tat Tyr	ttc Phe	577
aac Asn	ccc Pro	tca Ser 195	tct Ser	tct Ser	cac His	tca Ser	gct Ala 200	gly aaa	agg Arg	gac Asp	atg Met	gca Ala 205	gct Ala	gcc Ala	atg Met	625
					acc Thr											646
<21: <21: <21: <21:	1 > 2 2 > 1	421 215 PRT Mus 1	nuscı	ılus	dome	estio	cus									
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<22 AF0	3> 7398		n = :	1009:	2; c.	lone	= 0	R912	-47M	6; A	cces	sion	DDR	J/EM	BL/GenBan	ж =
	7398		n = :	1009:	2; c.	lone	= 01	R912	-47M	6; A	cces	sion	שטט	J/EM	BL/GenBan	ж =
AF0 <40	7398 0>	4 421			2; c.											к =
AF0 <40 Ser 1	7398 0> Val	4 421 Asp	Val	Cys 5		Ser	Ser	Thr	Thr 10	Val	Pro	Lys	Val	Leu 15	Ala	Κ =
AFO <40 Ser 1	7398 0> Val His	4 421 Asp Ile	Val Leu 20	Cys 5 Arg	Phe Asn Cys	Ser	Ser Ala	Thr Ile 25	Thr 10 Ser	Val Phe Met	Pro	Lys	Val Cys 30	Leu 15 Leu	Ala	Κ =
AF0 <40 Ser 1 Ile	7398 0> Val His Leu	4 421 Asp Ile Tyr 35	Val Leu 20	Cys 5 Arg Leu	Phe Asn Cys	Ser Gln Val	Ser Ala Phe	Thr Ile 25 Ala	Thr 10 Ser	Val Phe Met	Pro Ser Asp	Lys Gly Asn 45	Val Cys 30	Leu 15 Leu Leu	Ala Thr	κ =
AFO <40 Ser 1 Ile Gln Ala	7398 0> Val His Leu Val	4 421 Asp Ile Tyr 35 Met	Val Leu 20 Phe	Cys 5 Arg Leu	Phe Asn Cys Asp	Ser Gln Val Arg	Ser Ala Phe 40	Thr Ile 25 Ala Val	Thr 10 Ser Asp	Val Phe Met	Pro Ser Asp Cys	Lys Gly Asn 45	Val Cys 30 Phe	Leu 15 Leu Leu	Ala Thr Leu	K =
AFO <40 Ser 1 Ile Gln Ala Tyr 65	7398 0> Val His Leu Val 50	4 421 Asp Ile Tyr 35 Met	Val Leu 20 Phe Ala	Cys 5 Arg Leu Tyr	Phe Asn Cys Asp Thr	Ser Gln Val Arg 55	Ser Ala Phe 40 Phe	Thr Ile 25 Ala Val	Thr 10 Ser Asp Ala	Val Phe Met Ile	Pro Ser Asp Cys 60	Lys Gly Asn 45 His	Val Cys 30 Phe Pro	Leu 15 Leu Leu Val	Ala Thr Leu His	K =
AFO <40 Ser 1 Ile Gln Ala Tyr 65 Ser	7398 0> Val His Leu Val 50 Thr	4 421 Asp Ile Tyr 35 Met	Val Leu 20 Phe Ala Lys	Cys 5 Arg Leu Tyr Met Ala 85	Phe Asn Cys Asp Thr 70 Ser	Ser Gln Val Arg 55 His	Ser Ala Phe 40 Phe Gln	Thr Ile 25 Ala Val	Thr 10 Ser Asp Ala Cys Leu 90	Val Phe Met Ile Ala 75	Pro Ser Asp Cys 60	Lys Gly Asn 45 His	Val Cys 30 Phe Pro	Leu Leu Val Leu 95	Ala Thr Leu His	K =

115	120	125

Glu	Leu 130	Met	Ile	Leu	Ala	Val 135	Ala	Gly	Leu	Ile	Met 140	Leu	Ala	Pro	Phe	
Val 145	Cys	Ile	Leu	Leu	Ser 150	Tyr	Ile	Leu	Ile	Ala 155	Суз	Ala	Ile	Leu	Lys 160	
Ile	Ser	Ser	Thr	Gly 165	Arg	Trp	Lys	Ala	Phe 170	Ser	Thr	Cys	Gly	Ser 175	His	
Leu	Ala	Val	Val 180	Cys	Leu	Phe	Tyr	Gly 185	Thr	Ile	Ile	Ser	Leu 190	Tyr	Phe	
Asn	Pro	Ser 195	Ser	Ser	His	Ser	Ala 200	Gly	Arg	Asp	Met	Ala 205	Ala	Ala	Met	
Met	Tyr 210	Thr	Val	Val	Thr	Pro 215										
<210 <211 <212 <213	L> 6 2> I	122 550 ONA Mus m	nusci	ılus	dome	estio	cus									
<220 <221 <222 <223 AF07	L> r 2>		. (650	))	2; c]	lone	= OI	R912-	- 47M7	7; Ac	ccess	sion	DDB	J/EMI	3L/GenE	sank =
<220 <221 <222 <223 TM2	L> ( 2>				facto	ory 1	recel	ptor;	: reg	gion	betv	ween	tra	nsmer	mbrane	domains
<400 c tt Ph 1	t gt	122 Ig ga 11 As	ac at sp II	cc to le Cy 5	gt tt /s Pl	c ac ne Th	cc to	cc ac er Th	cc ac ir Th	nr Va	cc co	ca aa co Ly	ag at ys Me	ig ct et Le 15	tg gta eu Val	49
aat Asn	ata Ile	cag Gln	act Thr 20	caa Gln	agc Ser	aag Lys	gcc Ala	att Ile 25	aca Thr	tat Tyr	gca Ala	gac Asp	tgt Cys 30	att Ile	agc Ser	97
					ttg Leu											145
					gac Asp											193
					aac Asn 70											241

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser 85 90	Ser Ile Val 95
cta cag ttg acc ttt tgt gga gat gta aga att ccc cac Leu Gln Leu Thr Phe Cys Gly Asp Val Arg Ile Pro His 100 105	
gag ctt aac cag ctg tct caa ctc aca tgt tca gac agc Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser 115 120 125	
cac ctc ata atg cat ctt gta cct gtt cta ttg gga gcc His Leu Ile Met His Leu Val Pro Val Leu Leu Gly Ala 130 135 140	
agt agt atc ctt tac tct tat ttc aag ata gtg tcc tcc Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser 145 150 155	
atc tcc tca gtt caa ggg aag tac aag gca ttt tct aca Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr 165 170	
cac ctt tcc att gta tcc tta ttt tat agt aca ggc ctt His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu 180 185	
gtc agt tct gct gtg gtc caa agc tct cac tct gct gca Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala 195 200 205	
gtg atg tat act gtg gtc aca cac g Val Met Tyr Thr Val Val Thr His 210 215	650
<210> 423 <211> 216 <212> PRT <213> Mus musculus domesticus	
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Gln Met Ser Val Phe Leu Val Phe Gly Glu Leu Asp Asn 35 40 45	Phe Leu Leu
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His 50 55 60	Pro Leu Tyr

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val 85

70

Leu Gln Leu Thr Phe Cys Gly Asp Val Arg Ile Pro His Phe Phe Cys 105

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Leu Ser Ser 120

His Leu Ile Met His Leu Val Pro Val Leu Leu Gly Ala Ile Ser Phe 135 130

Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser 155 150

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 170

His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr

Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala Arg Ala Ser 200

Val Met Tyr Thr Val Val Thr His

<210> 424

<211> 649

<212> DNA <213> Mus musculus domesticus

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<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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97 aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser 25 20

cag atg tct gtc ttc ttg gtt ttt gca gaa ttg gac aac ttt ctc ctg 145

Gln	Met	Ser 35	Val	Phe	Leu	Val	Phe 40	Ala	Glu	Leu	Asp	Asn 45	Phe	Leu	Leu		
	gtg Val 50															19	3
	aca Thr															24	1
tcc Ser	tgg Trp	gtt Val	gtt Val	agc Ser 85	atc Ile	cta Leu	cat His	gcc Ala	ttc Phe 90	tta Leu	cag Gln	agc Ser	tca Ser	att Ile 95	gtg Val	28	9
cta Leu	cag Gln	ttg Leu	acc Thr 100	ttt Phe	tgt Cys	gga Gly	gat Asp	gta Val 105	aaa Lys	att Ile	ccc Pro	cac His	ttc Phe 110	ttc Phe	tgc Cys	33	7
gag Glu	ctt Leu	aac Asn 115	cag Gln	ctg Leu	tct Ser	caa Gln	ctc Leu 120	aca Thr	tgt Cys	tta Leu	gac Asp	agc Ser 125	ttt Phe	tca Ser	agc Ser	38	5
cac His	ctc Leu 130	ata Ile	atg Met	aat Asn	ctt Leu	gta Val 135	cct Pro	gtt Val	cta Leu	ttg Leu	gca Ala 140	gtc Val	att Ile	tcc Ser	ttc Phe	43	.3
agt Ser 145	agt Ser	atc Ile	ctt Leu	tac Tyr	tct Ser 150	tat Tyr	ttc Phe	aag Lys	ata Ile	gtg Val 155	tcc Ser	tcc Ser	ata Ile	tgt Cys	tct Ser 160	4.8	1
atc Ile	tcc Ser	tca Ser	gtt Val	caa Gln 165	Gly	aag Lys	tac Tyr	aag Lys	gca Ala 170	ttt Phe	tct Ser	aca Thr	tgt Cys	gtc Val 175	tct Ser	52	!9
cac His	ctt Leu	tcc Ser	att Ile 180	gtc Val	ttc Phe	tta Leu	ttt Phe	tat Tyr 185	agt Ser	aca Thr	ggc	ctt Leu	gga Gly 190	gtg Val	tat Tyr	57	17
gtc Val	agt Ser	tct Ser 195	Āla	gtg Val	gtc Val	caa Gln	agc Ser 200	tct Ser	cac His	tct Ser	gct Ala	gca Ala 205	aga Arg	gcc Ala	tct Ser	62	25
gtg Val	atg Met 210	tat Tyr	act Thr	gtg Val	gtc Val	acc Thr 215	ccg Pro									64	19
<21 <21 <21 <21	1 > 2 >	425 216 PRT Mus	musc	ulus	dom	esti	cus										
<22 <22 <22 <22 AF0	1 > 2 >	(1). Taxo	_fea .(64 n =	9)		lone	= 0	R912	-47M	8; A	cces	sion	DDB	J/EM	BL/Ge	enBank =	=
<40	0 >	425															
Phe 1	Val	Asp	Ile	Cys 5	Phe	Thr	Ser	Thr	Thr 10	Val	Pro	Lys	Val	Leu 15	Val		

Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser

Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr

Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val 85

Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys 105 100

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Leu Asp Ser Phe Ser Ser 120

His Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe

Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser 155

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 165

His Leu Ser Ile Val Phe Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr

Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala Arg Ala Ser 200

Val Met Tyr Thr Val Val Thr Pro

<210> 426 <211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc\_feature

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<221> CDS

<222> (2)..(649)

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cac ttc ctg His Phe Leu	gtg aag Val Lys 20	agg aag a Arg Lys T	cc att t hr Ile S 25	ect ttt g Ber Phe	gct gga Ala Gly	tgt tct a Cys Ser : 30	aca 97 Thr
cag ata gtg Gln Ile Val 35	gtg ttg Val Leu	ctt ctg g Leu Leu V 4	al Gly C	gc aca Cys Thr	gag tgt Glu Cys 45	gca ctg ( Ala Leu :	ctg 145 Leu
gca gtg atg Ala Val Met 50	tcc tat Ser Tyr	gac cga t Asp Arg T 55	at gtg g yr Val <i>F</i>	Ala Val	tgc aaa Cys Lys 60	cct ctg Pro Leu	cac 193 His
tac tcc acc Tyr Ser Thr 65	atc atg Ile Met	aca cac t Thr His T 70	gg cta t 'rp Leu (	tgt gtt Cys Val 75	cag ctg Gln Leu	Ala Ala	ggg 241 Gly 80
tcc tgg gcc Ser Trp Ala	agt ggt Ser Gly 85	gca ctt g Ala Leu V	al Ser	ctg gtg Leu Val 90	gat acc Asp Thr	aca ttc Thr Phe 95	aca 289 Thr
tta cgt ctt Leu Arg Leu	cct tat Pro Tyr 100	cga gga a Arg Gly A	aac aat q Asn Asn 105	gtc att Val Ile	aac cac Asn His	ttt ttc Phe Phe 110	tgt 337 Cys
gaa cct cct Glu Pro Pro 115	Ala Leu	Leu Lys I	ctg gca Leu Ala 120	tcg gca Ser Ala	gat aca Asp Thr 125	tac agc Tyr Ser	aca 385 Thr
gag atg gcg Glu Met Ala 130	g atc ttt a Ile Phe	gca atg g Ala Met 0 135	ggt gtg Gly Val	gta atc Val Ile	ctc cta Leu Leu 140	gca cct Ala Pro	gtc 433 Val
tcc ctc atc Ser Leu Ile 145	c ctc acc e Leu Thr	tcc tac t Ser Tyr 1	tgg aac Trp Asn	atc atc Ile Ile 155	tcc act Ser Thr	gta atc Val Ile	cag 481 Gln 160
atg cag tc Met Gln Se	ggg gaa Gly Glu 165	Gly Arg .	ctc aag Leu Lys	gtc ttc Val Phe 170	tcc acc Ser Thr	tgt ggc Cys Gly 175	tcc 529 Ser
cac ctc at	t gtt gtt e Val Val 180	gtt ctc Val Leu	ttc tac Phe Tyr 185	ggc tca Gly Ser	gca ata Ala Ile	ttt gcc Phe Ala 190	tac 577 Tyr
atg agg cc Met Arg Pr 19	o Asn Ser	Lys Ile	atg aat Met Asn 200	gaa aag Glu Lys	gat aaa Asp Lys 205	MEC IIC	tcg 625 Ser
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<222> (1)..(649)
<223> Taxon = 10092; clone = OR912-47M9; Accession DDBJ/EMBL/GenBank = AF073987

<400> 427

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His Phe Leu Val Lys Arg Lys Thr Ile Ser Phe Ala Gly Cys Ser Thr

Gln Ile Val Val Leu Leu Leu Val Gly Cys Thr Glu Cys Ala Leu Leu

Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys Pro Leu His 55

Tyr Ser Thr Ile Met Thr His Trp Leu Cys Val Gln Leu Ala Ala Gly 70

Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr Thr Phe Thr 85

Leu Arg Leu Pro Tyr Arg Gly Asn Asn Val Ile Asn His Phe Phe Cys

Glu Pro Pro Ala Leu Leu Lys Leu Ala Ser Ala Asp Thr Tyr Ser Thr

Glu Met Ala Ile Phe Ala Met Gly Val Val Ile Leu Leu Ala Pro Val

Ser Leu Ile Leu Thr Ser Tyr Trp Asn Ile Ile Ser Thr Val Ile Gln 145

Met Gln Ser Gly Glu Gly Arg Leu Lys Val Phe Ser Thr Cys Gly Ser

His Leu Ile Val Val Leu Phe Tyr Gly Ser Ala Ile Phe Ala Tyr 180

Met Arg Pro Asn Ser Lys Ile Met Asn Glu Lys Asp Lys Met Ile Ser 200

Val Phe Tyr Ser Ala Val Thr Pro

<210> 428 <211> 649

<212 <213		NA us m	uscu	lus	dome	stic	us									
<220 <221 <222 <223 <220 <221 <222	> m > ( > T	isc_ 1) axon DS 2)	(649 = 1	) 0092	; cl	one	= OR	.9M;	Acce	ssio	n DD	BJ/E	MBL/	GenB	ank =	AF073988
<223		rodu			acto	ry r	ecep	tor;	reg	ion	betw	een	tran	smem	brane	domains
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aac Asn	atg Met	cag Gln	agc Ser 20	caa Gln	gtt Val	cct Pro	tca Ser	atc Ile 25	ccc Pro	tat Tyr	gca Ala	ggc Gly	tgc Cys 30	ctg Leu	aca Thr	97
caa Gln	atg Met	tac Tyr 35	ttc Phe	ttt Phe	ttg Leu	ttt Phe	ttt Phe 40	gga Gly	gat Asp	ctt Leu	gag Glu	agc Ser 45	ttc Phe	ctc Leu	ctt Leu	145
gtg Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cga Arg 55	tat Tyr	gta Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctt Leu	cat His	193
tac Tyr 65	acc Thr	agc Ser	att Ile	atg Met	agc Ser 70	ccc Pro	agg Arg	ctc Leu	tgt Cys	gtg Val 75	agt Ser	ctt Leu	gtg Val	ctg Leu	ctg Leu 80	241
tcc Ser	tgg Trp	ttg Leu	ctg Leu	acc Thr 85	atg Met	tcc Ser	cat His	tcc Ser	atg Met 90	ctg Leu	cac His	act Thr	ttg Leu	ctc Leu 95	tta Leu	289
act Thr	agg Arg	ttg Leu	tct Ser 100	ttc Phe	tgt Cys	gaa Glu	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	337
gat Asp	ctg Leu	tct Ser 115	gct Ala	ctg Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn	385
gaa Glu	ttg Leu 130	gtg Val	ata Ile	ttg Leu	atc Ile	ata Ile 135	gga Gly	gly ggg	ctt Leu	gtt Val	gtt Val 140	ata Ile	ctt Leu	cca Pro	ttt Phe	433
cta Leu 145	ctc Leu	gtc Val	aca Thr	gtg Val	tct Ser 150	tat Tyr	gca Ala	cgc Arg	atc Ile	atc Ile 155	tcc Ser	tcc Ser	att Ile	ctc Leu	aag Lys 160	481
gtc Val	cct Pro	tca Ser	act Thr	cga Arg 165	ggc	atc Ile	cac His	aag Lys	gtc Val 170	ttc Phe	tcc Ser	act Thr	tgt Cys	ggt Gly 175	tct Ser	529
cac His	ctg Leu	tct Ser	gtg Val 180	Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly	aca Thr	att Ile	att Ile	ggc Gly 190	ctc Leu	tac Tyr	577
tta Leu	tgt Cys	cca Pro	tct Ser	gct Ala	aat Asn	aac Asn	tct Ser	Thr	cta Leu	aag Lys	gac Asp	act Thr	Val	atg Met	tct Ser	625

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<210> 429 <211> 216

<212> PRT

<213> Mus musculus domesticus

<220>

<221> misc feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR9M; Accession DDBJ/EMBL/GenBank = AF073988

<400> 429

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Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu 90 85

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 105 100

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 120 115

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe

Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 185

## Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 195

Leu Met Tyr Thr Val Val Thr Pro

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25 20 ttt ctg ctc atg ttt gtg gtc gct gtg ctt ggg aat ctt ctc atc att 684 Phe Leu Leu Met Phe Val Val Ala Val Leu Gly Asn Leu Leu Ile Ile ctg gcc gtc agc att gac tct cac ctg cat act ccc atg tac ttc ttt 732 Leu Ala Val Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe 55 50

Ser Gly Val Phe Gln Tyr Pro Glu His Gln Pro Met Leu Phe Gly Leu

780 cta tct aac ctg tcc ttt tct gac att ggt ttc atc tct aca act gtc Leu Ser Asn Leu Ser Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Val 70 828

cct aag atg ttg gtg aat atc caa aca cag agc aag tcc atc tcc tat Pro Lys Met Leu Val Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr 90 85 80

gca Ala 95	gaa Glu	tgc Cys	atc Ile	acc Thr	cag Gln 100	att Ile	tat Tyr	ttt Phe	ttc Phe	atg Met 105	ctc Leu	ttt Phe	gga Gly	ggc Gly	atg Met 110	876
gac Asp	aca Thr	ctt Leu	ctc Leu	ctc Leu 115	acc Thr	gtg Val	atg Met	gcc Ala	tat Tyr 120	gac Asp	cga Arg	ttt Phe	gtg Val	gcc Ala 125	atc Ile	924
tgt Cys	cac His	cca Pro	ctt Leu 130	cac His	tat Tyr	tca Ser	gtc Val	att Ile 135	atg Met	aat Asn	cct Pro	caa Gln	cta Leu 140	agt Ser	ggt Gly	972
ttg Leu	cta Leu	gtt Val 145	ctt Leu	gta Val	tca Ser	tgg Trp	ttt Phe 150	att Ile	agc Ser	ttt Phe	tca Ser	tat Tyr 155	tct Ser	ctg Leu	ata Ile	1020
cag Gln	agt Ser 160	cta Leu	ttg Leu	atg Met	ctg Leu	cgg Arg 165	ttg Leu	tcc Ser	ttc Phe	tgt Cys	aca Thr 170	aat Asn	cag Gln	ata Ile	att Ile	1068
aaa Lys 175	cac His	ttt Phe	tac Tyr	tgt Cys	gaa Glu 180	tat Tyr	gcc Ala	aaa Lys	gcc Ala	ctc Leu 185	act Thr	ata Ile	gcc Ala	tgc Cys	tca Ser 190	1116
gat Asp	aca Thr	cta Leu	atc Ile	aat Asn 195	cat His	atc Ile	ctt Leu	ctt Leu	tat Tyr 200	att Ile	gtg Val	ata Ile	tgg Trp	gtc Val 205	ctt Leu	1164
ggc Gly	ttc Phe	atc Ile	cct Pro 210	ttc Phe	tca Ser	Gly aaa	atc Ile	ctt Leu 215	tat Tyr	tca Ser	tac Tyr	tat Tyr	aaa Lys 220	att Ile	ttt Phe	1212
tct Ser	tca Ser	att Ile 225	ttg Leu	aga Arg	att Ile	cca Pro	tca Ser 230	aca Thr	gat Asp	gga Gly	aaa Lys	tat Tyr 235	aaa Lys	gca Ala	ttt Phe	1260
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ggc Gly 255	ctt Leu	agt Ser	gtg Val	tac Tyr	ctt Leu 260	agt Ser	tct Ser	gat Asp	gct Ala	act Thr 265	Ser	tcc Ser	tct Ser	ggg ggg	aag Lys 270	1356
ggc	gtg Val	gtg Val	gcc Ala	tca Ser 275	Val	atg Met	tat Tyr	aca Thr	gtg Val 280	Val	acc Thr	Pro	atg Met	ctg Leu 285	aac Asn	1404
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aca Thr	ctt Leu	999 Gly 305	Arg	ata Ile	ctt Leu	ctt Leu	tta Leu 310	. Lys	tga	. taa	tttc	act	ggtt	ttag	ac	1502
ato	tgaa	ctg	atag	jaaat	aa a	atag	tgaa	c ta	aaga	aatt	ctg	tact	ata	atca	tgtaga	1562
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cga	cata	ttt	cttt	actt	ca g	taca	aagt	c ta	catt	tcag	g cat	gcca	ata	taac	cattca	1742
aat	acca	att	cato	gaatt	gt t	tagt	aaaa	g tt	atgo	caato	g gct	catt	tac	agaa	agtcca	1802

tgta	tata	ta t	ataa	cact	g tt	gtgg	gttg	gto	cgac	tct	gtat	tctg	at a	ttaa	ttctg	1862
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Leu	Met	Phe 35	Val	Val	Ala	Val	Leu 40	Gly	Asn	Leu	Leu	Ile 45	Ile	Leu	Ala	
Val	Ser 50	Ile	Asp	Ser	His	Leu 55	His	Thr	Pro	Met	Tyr 60	Phe	Phe	Leu	Ser	
Asn 65	Leu	Ser	Phe	Ser	Asp 70	Ile	Gly	Phe	Ile	Ser 75	Thr	Thr	Val	Pro	Lys 80	
Met	Leu	Val	Asn	Ile 85	Gln	Thr	Gln	Ser	Lys 90	Ser	Ile	Ser	Tyr	Ala 95	Glu	
Cys	Ile	Thr	Gln 100	Ile	Tyr	Phe	Phe	Met 105	Leu	Phe	Gly	Gly	Met 110	Asp	Thr	
Leu	Leu	Leu 115	Thr	Val	Met	Ala	Tyr 120	Asp	Arg	Phe	Val	Ala 125	Ile	Сув	His	
Pro	Leu 130	His	Tyr	Ser	Val	Ile 135	Met	Asn	Pro	Gln	Leu 140	Ser	Gly	Leu	Leu	
Val 145		Val	Ser	Trp	Phe 150	Ile	Ser	Phe	Ser	Tyr 155	Ser	Leu	Ile	Gln	Ser 160	
Leu	Leu	Met	Leu	Arg 165		Ser	Phe	Суз	Thr 170	Asn	Gln	Ile	Ile	Lys 175	His	
Phe	Tyr	Сув	Glu 180		Ala	Lys	Ala	Leu 185		Ile	Ala	Сув	Ser 190	Asp	Thr	

IJ



Leu Ile Asn His Ile Leu Leu Tyr Ile Val Ile Trp Val Leu Gly Phe 195  $^{\prime}$   $^{\prime}$  200 205

Ile Pro Phe Ser Gly Ile Leu Tyr Ser Tyr Tyr Lys Ile Phe Ser Ser 210 215 220

Ile Leu Arg Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr 225 230 235 240

Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu 245 250 255

Ser Val Tyr Leu Ser Ser Asp Ala Thr Ser Ser Ser Gly Lys Gly Val 260 265 270

Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe 275 280 285

Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Lys Ala Leu Lys Thr Leu 290 295 300

Gly Arg Ile Leu Leu Leu Lys 305 310